SEQUENCE LISTING

<110> Sumitomo Chemical Co., Ltd.

<120> TRANSFORMED CELL WITH ENHANCED SENSITIVITY TO ANTIFUNGAL COMPOUN
D AND USE THEREOF

<130>

<160> 90

<210> 1

<211> 1315

<212> PRT

<213> Botryotinia fuckeliana

<400> 1

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Gly Ile Arg Leu Pro Gly Ala Asp Thr Ala Glu Lys Leu Ala Leu Glu
35 40 45

Arg Glu Leu Ala Ala Leu Val Ser Arg Val Gln Arg Leu Glu Ala Arg
50 55 60

Ala Ile Thr Val Asn Asn Gln Thr Leu Pro Asp Thr Pro Asn Glu Leu
65 70 75 80

Gly Ala Pro Ser Ala Phe Ala Asp Val Leu Thr Gly Ala Pro Ser Arg

85 90 95

Ala Ser Lys Ser Thr Thr Ser Arg Gln Gln Leu Val Asn Ser Leu Leu

100 105 110

Ala Ala Arg Glu Ala Pro Thr Gly Gly Glu Arg Pro Pro Lys Phe Thr

115 120 125

Lys Leu Ser Asp Glu Glu Leu Glu Ala Leu Arg Glu His Val Asp His

130 135 140

Gln Ser Lys Gln Leu Asp Ser Gln Lys Ser Glu Leu Ala Gly Val His

145 150 155 160

Ala Gln Leu Phe Glu Gln Lys Gln Arg Gln Glu Gln Ala Leu Asn Val

165 170 175

Leu Glu Val Glu Arg Val Ala Ala Leu Glu Arg Glu Leu Lys Lys His

180 185 190

Gln Gln Ala Asn Glu Ala Phe Gln Lys Ala Leu Arg Glu Ile Gly Glu

195 200 205

Ile Val Thr Ala Val Ala Arg Gly Asp Leu Ser Lys Lys Val Gln Ile

210 215 220

His Ser Val Glu Met Asp Pro Glu Ile Thr Thr Phe Lys Arg Val Ile

225 230 235 240

Asn Thr Met Met Asp Gln Leu Gln Ile Phe Ser Ser Glu Val Ser Arg

245 250 255

Val Ala Arg Glu Val Gly Thr Glu Gly Ile Leu Gly Gly Gln Ala Lys

260 265 270

Ile Ser Gly Val Asp Gly Thr Trp Lys Glu Leu Thr Asp Asn Val Asn

275 280 285

Val Met Ala Gln Asn Leu Thr Asp Gln Val Arg Glu Ile Ala Ser Val

290 295 300

Thr Thr Ala Val Ala His Gly Asp Leu Thr Gln Lys Ile Glu Arg Pro

305 310 315 320

Ala Gln Gly Glu Ile Leu Gln Leu Gln Gln Thr Ile Asn Thr Met Val

325 330 335

Asp Gln Leu Arg Thr Phe Ala Ala Glu Val Thr Arg Val Ala Arg Asp

340 345 350

Val Gly Thr Glu Gly Ile Leu Gly Gly Gln Ala Glu Ile Glu Gly Val

355 360 365

Gln Gly Met Trp Asn Thr Leu Ile Val Asn Val Asn Ala Met Ala Asn

370 375 380

Asn Leu Thr Thr Gln Val Arg Asp Ile Ala Ile Val Thr Thr Ala Val

385 390 395 400

Ala Lys Gly Asp Leu Thr Gln Lys Val Gln Ala Glu Cys Lys Gly Glu

405 410 415

Ile Lys Gln Leu Lys Glu Thr Ile Asn Ser Met Val Asp Gln Leu Gln

420 425 430

Gln Phe Ala Arg Glu Val Thr Lys Ile Ala Arg Glu Val Gly Thr Glu

435 440 445

Gly Arg Leu Gly Gly Gln Ala Thr Val His Asp Val Glu Gly Thr Trp

450 455 460

Arg Asp Leu Thr Glu Asn Val Asn Gly Met Ala Met Asn Leu Thr Thr

465 470 475 480

Gln Val Arg Glu Ile Ala Lys Val Thr Thr Ala Val Ala Arg Gly Asp

485 490 495

Leu Thr Lys Lys Ile Glu Val Glu Val Gln Gly Glu Ile Ala Ser Leu

500 505 510

Lys Asp Thr Ile Asn Thr Met Val Asp Arg Leu Ser Thr Phe Ala Phe

515 520 525

Glu Val Ser Lys Val Ala Arg Glu Val Gly Thr Asp Gly Thr Leu Gly

530 535 540

Gly Gln Ala Gln Val Asp Asn Val Glu Gly Lys Trp Lys Asp Leu Thr

545 550 555 560

Glu Asn Val Asn Thr Met Ala Arg Asn Leu Thr Thr Gln Val Arg Gly

565 570 575

Ile Ser Thr Val Thr Gln Ala Ile Ala Asn Gly Asp Met Ser Gln Lys

580 585 590

Ile Glu Val Ala Ala Ala Gly Glu Ile Leu Ile Leu Lys Glu Thr Ile

595 600 605

Asn Asn Met Val Asp Arg Leu Ser Ile Phe Ser Asn Glu Val Gln Arg

610 615 620

Val Ala Lys Asp Val Gly Val Asp Gly Lys Met Gly Gly Gln Ala Asp

625 630 635 640

Val Ala Gly Ile Gly Gly Arg Trp Lys Glu Ile Thr Thr Asp Val Asn

645 650 655

Thr Met Ala Asn Asn Leu Thr Thr Gln Val Arg Ala Phe Gly Asp Ile

660 665 670

Thr Asn Ala Ala Thr Asp Gly Asp Phe Thr Lys Leu Ile Thr Val Glu

675 680 685

Ala Ser Gly Glu Met Asp Glu Leu Lys Arg Lys Ile Asn Gln Met Val

690 695 700

Tyr Asn Leu Arg Asp Ser Ile Gln Arg Asn Thr Leu Ala Arg Glu Ala

705 710 715 720

Ala Glu Phe Ala Asn Arg Thr Lys Ser Glu Phe Leu Ala Asn Met Ser

725 730 735

His Glu Ile Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr Gln Leu

740 745 750

Thr Leu Asp Thr Asp Leu Thr Gln Tyr Gln Arg Glu Met Leu Asn Ile

755 760 765

Val His Asn Leu Ala Asn Ser Leu Leu Thr Ile Ile Asp Asp Ile Leu

770 775 780

Asp Leu Ser Lys Ile Glu Ala Asn Arg Met Ile Met Glu Glu Ile Pro

785 790 795 800

Tyr Thr Leu Arg Gly Thr Val Phe Asn Ala Leu Lys Thr Leu Ala Val

805 810 815

Lys Ala Asn Glu Lys Phe Leu Asp Leu Thr Tyr Arg Val Asp Ser Ser

820 825 830

Val Pro Asp His Val Val Gly Asp Ser Phe Arg Leu Arg Gln Val Ile

835 840 845

Leu Asn Leu Val Gly Asn Ala Ile Lys Phe Thr Glu His Gly Glu Val

850 855 860

Ser Leu Thr Ile Gln Lys Ala Glu Gln Asp His Cys Ala Pro Asn Glu

865 870 875 880

Tyr Ala Val Glu Phe Cys Val Ser Asp Thr Gly Ile Gly Ile Gln Ala

885 890 895

Asp Lys Leu Asn Leu Ile Phe Asp Thr Phe Gln Gln Ala Asp Gly Ser

900 905 910

Met Thr Arg Lys Phe Gly Gly Thr Gly Leu Gly Leu Ser Ile Ser Lys

915 920 925

Arg Leu Val Asn Leu Met Arg Gly Asp Val Trp Val Lys Ser Gln Tyr

930 935 940

Gly Lys Gly Ser Ser Phe Tyr Phe Thr Cys Thr Val Arg Leu Ala Thr

945 950 955 960

Ser Asp Ile Ser Phe Ile Gln Lys Gln Leu Lys Pro Tyr Gln Gly His

965 970 975

Asn Val Leu Phe Ile Asp Lys Gly Gln Thr Gly His Gly Lys Glu Ile

980 985 990

Ile Thr Met Leu Thr Gln Leu Gly Leu Val Pro Val Val Val Asp Ser

995 1000 1005

Glu Gln His Thr Ile Leu Leu Gly Asn Gly Arg Thr Lys Glu Lys Ile

1010 1015 1020

Ala Ser Thr Tyr Asp Val Ile Val Val Asp Ser Ile Glu Ser Ala Arg

1025 1030 1035 1040

Lys Leu Arg Ser Ile Asp Glu Phe Lys Tyr Ile Pro Ile Val Leu Leu

1045 1050 1055

Ala Pro Val Ile His Val Ser Leu Lys Ser Ala Leu Asp Leu Gly Ile

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Thr Ser Tyr Met Thr Thr Pro Cys Leu Thr Ile Asp Leu Gly Asn Gly

1075 1080 1085

Met Ile Pro Ala Leu Glu Asn Arg Ala Ala Pro Ser Leu Ala Asp Asn

1090 1095 1100

Thr Lys Ser Phe Asp Ile Leu Leu Ala Glu Asp Asn Ile Val Asn Gln

1105 1110 1115 1120

Arg Leu Ala Val Lys Ile Leu Glu Lys Tyr His His Val Val Thr Val

1125 1130 1135

Val Gly Asn Gly Gln Glu Ala Leu Asp Ala Ile Lys Glu Lys Arg Tyr

1140 1145 1150

Asp Val Ile Leu Met Asp Val Gln Met Pro Ile Met Gly Gly Phe Glu

1155 1160 1165

Ala Thr Ala Lys Ile Arg Glu Tyr Glu Arg Ser Leu Gly Thr Gln Arg

1170 1175 1180

Thr Pro Ile Ile Ala Leu Thr Ala His Ala Met Leu Gly Asp Arg Glu

1185 1190 1195 1200

Lys Cys Ile Gln Ala Gln Met Asp Glu Tyr Leu Ser Lys Pro Leu Lys

1205 1210 1215

Gln Asn His Leu Ile Gln Thr Ile Leu Lys Cys Ala Thr Leu Gly Gly

1220 1225 1230

Ala Leu Leu Glu Lys Gly Arg Glu Val Arg Gln Ser Ala Asn Glu Glu

1235 1240 1245

Ser Pro Asn Ser Gln Asn Gly Pro Arg Gly Thr Gln His Pro Ala Ser

1250 1255 1260

Ser Pro Thr Pro Ala His Met Arg Pro Ala Ile Glu Pro Arg Ala Tyr

1265 1270 1275 1280

Thr Thr Thr Gly Pro Ile Asn His Gly Ser Ala Glu Ser Pro Ser Leu

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His Ser Ser

1315

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<212> DNA

<213> Botryotinia fuckeliana

<220>

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Ala Leu Ser Ser Ile Asp Leu Pro Leu Thr Asn Val Tyr Gly Asn Lys
20 25 30

ggg att agg tta cca ggt gca gat acg gca gag aag ctt gcc ctc gaa 144
Gly Ile Arg Leu Pro Gly Ala Asp Thr Ala Glu Lys Leu Ala Leu Glu
35 40 45

cga gaa ctt gcg gcc ttg gta tcc aga gtc caa aga tta gaa gca agg 192
Arg Glu Leu Ala Ala Leu Val Ser Arg Val Gln Arg Leu Glu Ala Arg
50 55 60

gcg atc aca gtc aat aat caa acc ctg ccc gat acg ccg aat gaa tta 240
Ala Ile Thr Val Asn Asn Gln Thr Leu Pro Asp Thr Pro Asn Glu Leu
65 70 75 80

gga gcg cca tct gct ttc gca gat gta ctc act ggt gcc cca tcc cga 288
Gly Ala Pro Ser Ala Phe Ala Asp Val Leu Thr Gly Ala Pro Ser Arg
85 90 95

gcc tca aag agt act aca tcc cga caa cag ctc gta aat tcg ttg ctt 336
Ala Ser Lys Ser Thr Thr Ser Arg Gln Gln Leu Val Asn Ser Leu Leu
100 105 110

gcc gcc aga gaa gcg ccc acc ggc ggt gaa aga cct cct aaa ttt acg 384
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115 120 125

aaa tta agt gac gag gaa ctc gaa gca ctc cgc gaa cat gtc gac cat 432
Lys Leu Ser Asp Glu Glu Leu Glu Ala Leu Arg Glu His Val Asp His
130 135 140

caa tcg aaa caa ctc gat agt caa aaa tct gag ctg gcc ggt gta cat 480
Gln Ser Lys Gln Leu Asp Ser Gln Lys Ser Glu Leu Ala Gly Val His
145 150 155 160

gct caa ctg ttt gag cag aag cag aga caa gaa caa gca ctc aac gtt 528

Ala Gln Leu Phe Glu Gln Lys Gln Arg Gln Glu Gln Ala Leu Asn Val
165 170 175

ctt gaa gtc gaa cgc gta gca gct ctc gaa aga gaa ctg aag aag cat 576
Leu Glu Val Glu Arg Val Ala Ala Leu Glu Arg Glu Leu Lys Lys His
180 185 190

caa caa gcc aac gag gct ttc caa aaa gct cta cgg gaa ata gga gag 624
Gln Gln Ala Asn Glu Ala Phe Gln Lys Ala Leu Arg Glu Ile Gly Glu
195 200 205

att gtc aca gct gta gct agg ggt gat ctc agt aag aag gta caa atc 672
Ile Val Thr Ala Val Ala Arg Gly Asp Leu Ser Lys Lys Val Gln Ile
210 215 220

cac tcc gtg gag atg gac cct gag att aca act ttc aag cgt gtt att 720
His Ser Val Glu Met Asp Pro Glu Ile Thr Thr Phe Lys Arg Val Ile
225 230 235 240

aat act atg atg gat caa ctt cag ata ttc tct agt gag gtt tct cgt 768
Asn Thr Met Met Asp Gln Leu Gln Ile Phe Ser Ser Glu Val Ser Arg
245 250 255

gta gct aga gag gtc ggc aca gaa ggt att ctc ggt gga caa gcc aag 816
Val Ala Arg Glu Val Gly Thr Glu Gly Ile Leu Gly Gly Gln Ala Lys
260 265 270

att tct ggt gtt gat ggt aca tgg aag gag ttg act gac aat gtc aac 864
Ile Ser Gly Val Asp Gly Thr Trp Lys Glu Leu Thr Asp Asn Val Asn
275 280 285

gtt atg gca caa aat ctc acc gat caa gtc cga gaa att gct tcc gtc 912
Val Met Ala Gln Asn Leu Thr Asp Gln Val Arg Glu Ile Ala Ser Val
290 295 300

act act gct gta gct cat gga gat ctc aca caa aag att gag aga cca 960
Thr Thr Ala Val Ala His Gly Asp Leu Thr Gln Lys Ile Glu Arg Pro
305 310 315 320

gcc cag ggt gag ata ctc caa ctg caa caa act atc aat acc atg gtg 1008
Ala Gln Gly Glu Ile Leu Gln Leu Gln Gln Thr Ile Asn Thr Met Val
325 330 335

gat caa ttg aga acg ttc gcc gcc gag gtc acc cgc gta gca aga gat 1056
Asp Gln Leu Arg Thr Phe Ala Ala Glu Val Thr Arg Val Ala Arg Asp
340 345 350

gta gga act gaa ggt att ctt ggg ggt caa gca gaa atc gaa ggc gtc 1104
Val Gly Thr Glu Gly Ile Leu Gly Gly Gln Ala Glu Ile Glu Gly Val
355 360 365

cag ggc atg tgg aac aca ttg ata gtg aac gtc aac gct atg gcc aat 1152

Gln Gly Met Trp Asn Thr Leu Ile Val Asn Val Asn Ala Met Ala Asn
370 375 380

aac ctc acc aca caa gtg cgc gat ata gcc att gtc aca aca gct gtc 1200
Asn Leu Thr Thr Gln Val Arg Asp Ile Ala Ile Val Thr Thr Ala Val
385 390 395 400

gca aag gga gac ctg act caa aag gtc caa gca gaa tgt aag ggt gaa 1248
Ala Lys Gly Asp Leu Thr Gln Lys Val Gln Ala Glu Cys Lys Gly Glu
405 410 415

atc aag cag ttg aag gag act ata aat tcc atg gtg gac caa tta caa 1296
Ile Lys Gln Leu Lys Glu Thr Ile Asn Ser Met Val Asp Gln Leu Gln
420 425 430

caa ttt gcg cga gaa gtc acg aag att gct agg gag gtc ggt acc gaa 1344
Gln Phe Ala Arg Glu Val Thr Lys Ile Ala Arg Glu Val Gly Thr Glu
435 440 445

ggt aga ctg ggt gga caa gca aca gtg cat gat gtt gaa ggc act tgg 1392
Gly Arg Leu Gly Gly Gln Ala Thr Val His Asp Val Glu Gly Thr Trp
450 455 460

aga gac ctc acc gaa aat gtg aat ggt atg gcc atg aat ctt acg aca 1440
Arg Asp Leu Thr Glu Asn Val Asn Gly Met Ala Met Asn Leu Thr Thr
465 470 475 480

caa gta cga gag att gca aag gtt acc acc gct gtc gcc aga gga gat 1488
Gln Val Arg Glu Ile Ala Lys Val Thr Thr Ala Val Ala Arg Gly Asp
485 490 495

ttg acc aag aag att gaa gtc gag gtt cag gga gaa atc gct tcg ctg 1536
Leu Thr Lys Lys Ile Glu Val Glu Val Gln Gly Glu Ile Ala Ser Leu
500 505 510

aaa gat acc atc aac acc atg gtg gac aga ctt agt aca ttc gct ttt 1584
Lys Asp Thr Ile Asn Thr Met Val Asp Arg Leu Ser Thr Phe Ala Phe
515 520 525

gag gtt agc aaa gtc gcc agg gag gtc gga act gat ggg act ctt ggt 1632
Glu Val Ser Lys Val Ala Arg Glu Val Gly Thr Asp Gly Thr Leu Gly
530 535 540

gga caa gcg caa gtt gat aac gtc gaa gga aag tgg aaa gac ctc act 1680
Gly Gln Ala Gln Val Asp Asn Val Glu Gly Lys Trp Lys Asp Leu Thr
545 550 555 560

gaa aat gtg aac acc atg gcc aga aac ttg act act caa gta cga ggt 1728
Glu Asn Val Asn Thr Met Ala Arg Asn Leu Thr Thr Gln Val Arg Gly
565 570 575

atc tcg act gtt aca caa gct att gcc aat gga gac atg agt cag aag 1776

Ile Ser Thr Val Thr Gln Ala Ile Ala Asn Gly Asp Met Ser Gln Lys
580 585 590

att gag gtt gct gct gcg ggt gaa ata ctc ata cta aag gaa acc ata 1824
Ile Glu Val Ala Ala Ala Gly Glu Ile Leu Ile Leu Lys Glu Thr Ile
595 600 605

aat aac atg gta gac aga ttg agt atc ttc tcc aac gaa gtg caa aga 1872
Asn Asn Met Val Asp Arg Leu Ser Ile Phe Ser Asn Glu Val Gln Arg
610 615 620

gtc gcc aaa gat gtg ggt gtg gat ggt aag atg ggt ggc caa gct gac 1920
Val Ala Lys Asp Val Gly Val Asp Gly Lys Met Gly Gly Gln Ala Asp
625 630 635 640

gtt gct ggg att ggc ggc cgt tgg aaa gag atc aca acg gat gtc aat 1968
Val Ala Gly Ile Gly Gly Arg Trp Lys Glu Ile Thr Thr Asp Val Asn
645 650 655

acc atg gct aac aac ttg aca acc caa gtg cgc gcc ttt ggt gat ata 2016
Thr Met Ala Asn Asn Leu Thr Thr Gln Val Arg Ala Phe Gly Asp Ile
660 665 670

act aac gcc gca acc gat ggc gac ttc aca aaa ttg atc act gtc gag 2064
Thr Asn Ala Ala Thr Asp Gly Asp Phe Thr Lys Leu Ile Thr Val Glu
675 680 685

gca tct gga gag atg gat gag ctg aag cga aag atc aac cag atg gtg 2112
Ala Ser Gly Glu Met Asp Glu Leu Lys Arg Lys Ile Asn Gln Met Val
690 695 700

tac aat ctg agg gac agt att caa aga aac acc ttg gct agg gag gct 2160
Tyr Asn Leu Arg Asp Ser Ile Gln Arg Asn Thr Leu Ala Arg Glu Ala
705 710 715 720

gcc gaa ttc gcc aat agg acg aag tct gaa ttc ttg gct aac atg tct 2208
Ala Glu Phe Ala Asn Arg Thr Lys Ser Glu Phe Leu Ala Asn Met Ser
725 730 735

cac gag att cga aca cct atg aac ggt atc att ggt atg act cag ttg 2256
His Glu Ile Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr Gln Leu
740 745 750

aca ctc gac acc gat ctt act caa tat caa cga gaa atg ctc aac att 2304
Thr Leu Asp Thr Asp Leu Thr Gln Tyr Gln Arg Glu Met Leu Asn Ile
755 760 765

gtt cac aac ttg gcc aac agt tta ttg acc atc att gat gat att ctc 2352
Val His Asn Leu Ala Asn Ser Leu Leu Thr Ile Ile Asp Asp Ile Leu
770 775 780

gat tta tca aag atc gaa gca aac cgt atg atc atg gag gag att cca 2400

Asp Leu Ser Lys Ile Glu Ala Asn Arg Met Ile Met Glu Glu Ile Pro
785 790 795 800

tac act ctt aga gga acc gtc ttc aac gcc ctc aag act ctc gct gtc 2448
Tyr Thr Leu Arg Gly Thr Val Phe Asn Ala Leu Lys Thr Leu Ala Val
805 810 815

aag gca aat gag aag ttc cta gac ctc act tac cgc gta gat agc tca 2496
Lys Ala Asn Glu Lys Phe Leu Asp Leu Thr Tyr Arg Val Asp Ser Ser
820 825 830

gtt cca gat cac gtg gtt ggt gat tca ttc cgt ctt cga caa gtt att 2544
Val Pro Asp His Val Val Gly Asp Ser Phe Arg Leu Arg Gln Val Ile
835 840 845

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Leu Asn Leu Val Gly Asn Ala Ile Lys Phe Thr Glu His Gly Glu Val
850 855 860

tcg ttg acc atc caa aaa gcc gag caa gat cat tgt gcg ccg aac gaa 2640
Ser Leu Thr Ile Gln Lys Ala Glu Gln Asp His Cys Ala Pro Asn Glu
865 870 875 880

tat gca gtc gag ttt tgt gtt tct gac act ggt atc ggt atc caa gct 2688
Tyr Ala Val Glu Phe Cys Val Ser Asp Thr Gly Ile Gly Ile Gln Ala
885 890 895

gat aag ctc aat ttg att ttc gac act ttc caa caa gct gac gga tct 2736
Asp Lys Leu Asn Leu Ile Phe Asp Thr Phe Gln Gln Ala Asp Gly Ser
900 905 910

atg acg agg aaa ttc gga ggt act ggt cta ggt cta tca att tcg aag 2784
Met Thr Arg Lys Phe Gly Gly Thr Gly Leu Gly Leu Ser Ile Ser Lys
915 920 925

aga ctt gta aac ctc atg cgt gga gat gtt tgg gtt aag agt cag tac 2832
Arg Leu Val Asn Leu Met Arg Gly Asp Val Trp Val Lys Ser Gln Tyr
930 935 940

gga aaa ggc agt tca ttc tac ttc acg tgt acc gtc cgc ctc gca acc 2880
Gly Lys Gly Ser Ser Phe Tyr Phe Thr Cys Thr Val Arg Leu Ala Thr
945 950 955 960

tca gat atc agt ttc att cag aaa caa ctc aag cca tat caa ggt cac 2928
Ser Asp Ile Ser Phe Ile Gln Lys Gln Leu Lys Pro Tyr Gln Gly His
965 970 975

aat gtt ttg ttt atc gac aaa gga cag act ggc cat ggc aaa gaa ata 2976
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980 985 990

atc act atg ctt aca caa ctt ggt ttg gta ccc gtt gtt gtt gac tct 3024

Ile Thr Met Leu Thr Gln Leu Gly Leu Val Pro Val Val Val Asp Ser
995 1000 1005

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Glu Gln His Thr Ile Leu Leu Gly Asn Gly Arg Thr Lys Glu Lys Ile
1010 1015 1020

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1025 1030 1035 1040

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Lys Leu Arg Ser Ile Asp Glu Phe Lys Tyr Ile Pro Ile Val Leu Leu
1045 1050 1055

gct ccc gtt att cat gtc agc tta aag tct gct ttg gat ctt ggt atc 3216
Ala Pro Val Ile His Val Ser Leu Lys Ser Ala Leu Asp Leu Gly Ile
1060 1065 1070

act tct tac atg acc act cca tgt tta acg atc gat ctt ggc aat ggt 3264
Thr Ser Tyr Met Thr Thr Pro Cys Leu Thr Ile Asp Leu Gly Asn Gly
1075 1080 1085

atg att cct gct ttg gag aat cga gct gca ccc tca ttg gcg gac aac 3312
Met Ile Pro Ala Leu Glu Asn Arg Ala Ala Pro Ser Leu Ala Asp Asn
1090 1095 1100

aca aaa tcc ttc gac att ctc ttg gcc gaa gat aac atc gtc aat caa 3360
Thr Lys Ser Phe Asp Ile Leu Leu Ala Glu Asp Asn Ile Val Asn Gln
1105 1110 1115 1120

cgc tta gcg gtg aag att cta gaa aag tat cac cac gtc gtc aca gtc 3408
Arg Leu Ala Val Lys Ile Leu Glu Lys Tyr His His Val Val Thr Val
1125 1130 1135

gtt ggc aat ggt caa gaa gca cta gat gct atc aag gag aaa cga tac 3456
Val Gly Asn Gly Gln Glu Ala Leu Asp Ala Ile Lys Glu Lys Arg Tyr
1140 1145 1150

gat gtt att ctc atg gac gtt caa atg cca att atg gga gga ttc gaa 3504
Asp Val Ile Leu Met Asp Val Gln Met Pro Ile Met Gly Gly Phe Glu
1155 1160 1165

gca acc gct aag att aga gag tac gaa cgg agt ctt gga acg caa aga 3552
Ala Thr Ala Lys Ile Arg Glu Tyr Glu Arg Ser Leu Gly Thr Gln Arg
1170 1175 1180

acg cct att atc gca ctt aca gca cac gct atg ttg ggt gat cgc gaa 3600
Thr Pro Ile Ile Ala Leu Thr Ala His Ala Met Leu Gly Asp Arg Glu
1185 1190 1195 1200

aaa tgt att caa gcc caa atg gat gaa tat ctt tct aag cct ctg aaa 3648

Lys Cys Ile Gln Ala Gln Met Asp Glu Tyr Leu Ser Lys Pro Leu Lys
1205 1210 1215

caa aat cat ctt att cag acg atc ttg aaa tgt gca acc ctt gga ggt 3696
Gln Asn His Leu Ile Gln Thr Ile Leu Lys Cys Ala Thr Leu Gly Gly
1220 1225 1230

gca ttg ctc gag aag ggt agg gag gtt agg caa tcc gct aat gaa gag 3744
Ala Leu Leu Glu Lys Gly Arg Glu Val Arg Gln Ser Ala Asn Glu Glu
1235 1240 1245

agc ccc aat tcg caa aat ggt cct cgc ggt aca cag cat cct gca tca 3792
Ser Pro Asn Ser Gln Asn Gly Pro Arg Gly Thr Gln His Pro Ala Ser
1250 1255 1260

agt ccc aca cca gcc cat atg aga ccg gct atc gaa cct cgt gca tac 3840
Ser Pro Thr Pro Ala His Met Arg Pro Ala Ile Glu Pro Arg Ala Tyr
1265 1270 1275 1280

acg acc act ggc cct ata aat cat gga agt gca gag agt cct tca ctt 3888
Thr Thr Thr Gly Pro Ile Asn His Gly Ser Ala Glu Ser Pro Ser Leu
1285 1290 1295

gta acg gca gat gct gag gat cca ctt gcg agg ctt cta atg cgt gcg 3936
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cat agc agc tag 3948

His Ser Ser

1315

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<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed oligonucleotide primer for PCR

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<210> 4

<211> 33

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Designed

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<210> 5

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed oligonucleotide primer for sequencing

<400> 5

gatgtactca ctggtgcccc atcccgagcc 30

<210> 6

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed

oligonucleotide primer for sequencing

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ctcaaacagt tgagcatgta caccggccag 30

<210> 7

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Designed
oligonucleotide primer for sequencing

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acagaaggta ttctcggtgg acaagccaag 30

<210> 8

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Designed

oligonucleotide primer for sequencing

<400> 8

gctagggagg tcggtaccga aggtagactg 30

<210> 9

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for sequencing

<400> 9

atcttctcca acgaagtgca aagagtcgcc 30

<210> 10

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed

oligonucleotide primer for sequencing

<400> 10

gaggagattc catacactct tagaggaacc 30

<210> 11

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for sequencing

<400> 11

atcgacaaag gacagactgg ccatggc 27

<210> 12

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed

oligonucleotide primer for sequencing

<400> 12

atgccaatta tgggaggatt cgaagcaacc 30

<210> 13

<211> 1315

<212> PRT

<213> Botryotinia fuckeliana

<400> 13

Met Glu Asp Ser Thr Ile Ala His Thr Thr Ala Ile Leu Gln Thr Leu
1 5 10 15

Ala Leu Ser Ser Ile Asp Leu Pro Leu Thr Asn Val Tyr Gly Asn Lys
20 25 30

Gly Ile Arg Leu Pro Gly Ala Asp Thr Ala Glu Lys Leu Ala Leu Glu
35 40 45

Arg Glu Leu Ala Ala Leu Val Ser Arg Val Gln Arg Leu Glu Ala Arg
50 55 60

Ala Ile Thr Val Asn Asn Gln Thr Leu Pro Asp Thr Pro Asn Glu Leu
65 70 75 80

Gly Ala Pro Ser Ala Phe Ala Asp Val Leu Thr Gly Ala Pro Ser Arg
85 90 95

Ala Ser Lys Ser Thr Thr Ser Arg Gln Gln Leu Val Asn Ser Leu Leu
100 105 110

Ala Ala Arg Glu Ala Pro Thr Gly Gly Glu Arg Pro Pro Lys Phe Thr
115 120 125
Lys Leu Ser Asp Glu Glu Leu Glu Ala Leu Arg Glu His Val Asp His
130 135 140
Gln Ser Lys Gln Leu Asp Ser Gln Lys Ser Glu Leu Ala Gly Val His
145 150 155 160
Ala Gln Leu Phe Glu Gln Lys Gln Arg Gln Glu Gln Ala Leu Asn Val
165 170 175
Leu Glu Val Glu Arg Val Ala Ala Leu Glu Arg Glu Leu Lys Lys His
180 185 190
Gln Gln Ala Asn Glu Ala Phe Gln Lys Ala Leu Arg Glu Ile Gly Glu
195 200 205
Ile Val Thr Ala Val Ala Arg Gly Asp Leu Ser Lys Lys Val Gln Ile
210 215 220
His Ser Val Glu Met Asp Pro Glu Ile Thr Thr Phe Lys Arg Val Ile
225 230 235 240
Asn Thr Met Met Asp Gln Leu Gln Ile Phe Ser Ser Glu Val Ser Arg
245 250 255
Val Ala Arg Glu Val Gly Thr Glu Gly Ile Leu Gly Gly Gln Ala Lys
260 265 270
Ile Ser Gly Val Asp Gly Thr Trp Lys Glu Leu Thr Asp Asn Val Asn
275 280 285
Val Met Ala Gln Asn Leu Thr Asp Gln Val Arg Glu Ile Ala Ser Val
290 295 300
Thr Thr Ala Val Ala His Gly Asp Leu Thr Gln Lys Ile Glu Arg Pro
305 310 315 320

Ala Gln Gly Glu Ile Leu Gln Leu Gln Gln Thr Ile Asn Thr Met Val
325 330 335
Asp Gln Leu Arg Thr Phe Ala Ala Glu Val Thr Arg Val Ala Arg Asp
340 345 350
Val Gly Thr Glu Gly Ile Leu Gly Gly Gln Ala Glu Ser Glu Gly Val
355 360 365
Gln Gly Met Trp Asn Thr Leu Ile Val Asn Val Asn Ala Met Ala Asn
370 375 380
Asn Leu Thr Thr Gln Val Arg Asp Ile Ala Ile Val Thr Thr Ala Val
385 390 395 400
Ala Lys Gly Asp Leu Thr Gln Lys Val Gln Ala Glu Cys Lys Gly Glu
405 410 415
Ile Lys Gln Leu Lys Glu Thr Ile Asn Ser Met Val Asp Gln Leu Gln
420 425 430
Gln Phe Ala Arg Glu Val Thr Lys Ile Ala Arg Glu Val Gly Thr Glu
435 440 445
Gly Arg Leu Gly Gly Gln Ala Thr Val His Asp Val Glu Gly Thr Trp
450 455 460
Arg Asp Leu Thr Glu Asn Val Asn Gly Met Ala Met Asn Leu Thr Thr
465 470 475 480
Gln Val Arg Glu Ile Ala Lys Val Thr Thr Ala Val Ala Arg Gly Asp
485 490 495
Leu Thr Lys Lys Ile Glu Val Glu Val Gln Gly Glu Ile Ala Ser Leu
500 505 510
Lys Asp Thr Ile Asn Thr Met Val Asp Arg Leu Ser Thr Phe Ala Phe
515 520 525

Glu Val Ser Lys Val Ala Arg Glu Val Gly Thr Asp Gly Thr Leu Gly
530 535 540
Gly Gln Ala Gln Val Asp Asn Val Glu Gly Lys Trp Lys Asp Leu Thr
545 550 555 560
Glu Asn Val Asn Thr Met Ala Arg Asn Leu Thr Thr Gln Val Arg Gly
565 570 575
Ile Ser Thr Val Thr Gln Ala Ile Ala Asn Gly Asp Met Ser Gln Lys
580 585 590
Ile Glu Val Ala Ala Ala Gly Glu Ile Leu Ile Leu Lys Glu Thr Ile
595 600 605
Asn Asn Met Val Asp Arg Leu Ser Ile Phe Ser Asn Glu Val Gln Arg
610 615 620
Val Ala Lys Asp Val Gly Val Asp Gly Lys Met Gly Gly Gln Ala Asp
625 630 635 640
Val Ala Gly Ile Gly Gly Arg Trp Lys Glu Ile Thr Thr Asp Val Asn
645 650 655
Thr Met Ala Asn Asn Leu Thr Thr Gln Val Arg Ala Phe Gly Asp Ile
660 665 670
Thr Asn Ala Ala Thr Asp Gly Asp Phe Thr Lys Leu Ile Thr Val Glu
675 680 685
Ala Ser Gly Glu Met Asp Glu Leu Lys Arg Lys Ile Asn Gln Met Val
690 695 700
Tyr Asn Leu Arg Asp Ser Ile Gln Arg Asn Thr Leu Ala Arg Glu Ala
705 710 715 720
Ala Glu Phe Ala Asn Arg Thr Lys Ser Glu Phe Leu Ala Asn Met Ser
725 730 735

His Glu Ile Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr Gln Leu
740 745 750

Thr Leu Asp Thr Asp Leu Thr Gln Tyr Gln Arg Glu Met Leu Asn Ile
755 760 765

Val His Asn Leu Ala Asn Ser Leu Leu Thr Ile Ile Asp Asp Ile Leu
770 775 780

Asp Leu Ser Lys Ile Glu Ala Asn Arg Met Ile Met Glu Glu Ile Pro
785 790 795 800

Tyr Thr Leu Arg Gly Thr Val Phe Asn Ala Leu Lys Thr Leu Ala Val
805 810 815

Lys Ala Asn Glu Lys Phe Leu Asp Leu Thr Tyr Arg Val Asp Ser Ser
820 825 830

Val Pro Asp His Val Val Gly Asp Ser Phe Arg Leu Arg Gln Val Ile
835 840 845

Leu Asn Leu Val Gly Asn Ala Ile Lys Phe Thr Glu His Gly Glu Val
850 855 860

Ser Leu Thr Ile Gln Lys Ala Glu Gln Asp His Cys Ala Pro Asn Glu
865 870 875 880

Tyr Ala Val Glu Phe Cys Val Ser Asp Thr Gly Ile Gly Ile Gln Ala
885 890 895

Asp Lys Leu Asn Leu Ile Phe Asp Thr Phe Gln Gln Ala Asp Gly Ser
900 905 910

Met Thr Arg Lys Phe Gly Gly Thr Gly Leu Gly Leu Ser Ile Ser Lys
915 920 925

Arg Leu Val Asn Leu Met Arg Gly Asp Val Trp Val Lys Ser Gln Tyr
930 935 940

Gly Lys Gly Ser Ser Phe Tyr Phe Thr Cys Thr Val Arg Leu Ala Thr
945 950 955 960
Ser Asp Ile Ser Phe Ile Gln Lys Gln Leu Lys Pro Tyr Gln Gly His
965 970 975
Asn Val Leu Phe Ile Asp Lys Gly Gln Thr Gly His Gly Lys Glu Ile
980 985 990
Ile Thr Met Leu Thr Gln Leu Gly Leu Val Pro Val Val Val Asp Ser
995 1000 1005
Glu Gln His Thr Ile Leu Leu Gly Asn Gly Arg Thr Lys Glu Lys Ile
1010 1015 1020
Ala Ser Thr Tyr Asp Val Ile Val Val Asp Ser Ile Glu Ser Ala Arg
1025 1030 1035 1040
Lys Leu Arg Ser Ile Asp Glu Phe Lys Tyr Ile Pro Ile Val Leu Leu
1045 1050 1055
Ala Pro Val Ile His Val Ser Leu Lys Ser Ala Leu Asp Leu Gly Ile
1060 1065 1070
Thr Ser Tyr Met Thr Thr Pro Cys Leu Thr Ile Asp Leu Gly Asn Gly
1075 1080 1085
Met Ile Pro Ala Leu Glu Asn Arg Ala Ala Pro Ser Leu Ala Asp Asn
1090 1095 1100
Thr Lys Ser Phe Asp Ile Leu Leu Ala Glu Asp Asn Ile Val Asn Gln
1105 1110 1115 1120
Arg Leu Ala Val Lys Ile Leu Glu Lys Tyr His His Val Val Thr Val
1125 1130 1135
Val Gly Asn Gly Gln Glu Ala Leu Asp Ala Ile Lys Glu Lys Arg Tyr
1140 1145 1150

Asp Val Ile Leu Met Asp Val Gln Met Pro Ile Met Gly Gly Phe Glu
1155 1160 1165

Ala Thr Ala Lys Ile Arg Glu Tyr Glu Arg Ser Leu Gly Thr Gln Arg
1170 1175 1180

Thr Pro Ile Ile Ala Leu Thr Ala His Ala Met Leu Gly Asp Arg Glu
1185 1190 1195 1200

Lys Cys Ile Gln Ala Gln Met Asp Glu Tyr Leu Ser Lys Pro Leu Lys
1205 1210 1215

Gln Asn His Leu Ile Gln Thr Ile Leu Lys Cys Ala Thr Leu Gly Gly
1220 1225 1230

Ala Leu Leu Glu Lys Gly Arg Glu Val Arg Gln Ser Ala Asn Glu Glu
1235 1240 1245

Ser Pro Asn Ser Gln Asn Gly Pro Arg Gly Thr Gln His Pro Ala Ser
1250 1255 1260

Ser Pro Thr Pro Ala His Met Arg Pro Ala Ile Glu Pro Arg Ala Tyr
1265 1270 1275 1280

Thr Thr Thr Gly Pro Ile Asn His Gly Ser Ala Glu Ser Pro Ser Leu
1285 1290 1295

Val Thr Ala Asp Ala Glu Asp Pro Leu Ala Arg Leu Leu Met Arg Ala
1300 1305 1310

His Ser Ser
1315

<210> 14

<211> 3948

<212> DNA

<213> Botryotinia fuckeliana

<220>

<221> CDS

<222> (1)..(3948)

<400> 14

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Met Glu Asp Ser Thr Ile Ala His Thr Thr Ala Ile Leu Gln Thr Leu
1 5 10 15

gca tta tcg agc atc gat ctt cca ctg acg aat gtt tac ggc aac aag 96
Ala Leu Ser Ser Ile Asp Leu Pro Leu Thr Asn Val Tyr Gly Asn Lys
20 25 30

ggg att agg tta cca ggt gca gat acg gca gag aag ctt gcc ctc gaa 144
Gly Ile Arg Leu Pro Gly Ala Asp Thr Ala Glu Lys Leu Ala Leu Glu
35 40 45

cga gaa ctt gcg gcc ttg gta tcc aga gtc caa aga tta gaa gca agg 192
Arg Glu Leu Ala Ala Leu Val Ser Arg Val Gln Arg Leu Glu Ala Arg
50 55 60

gcg atc aca gtc aat aat caa acc ctg ccc gat acg ccg aat gaa tta 240
Ala Ile Thr Val Asn Asn Gln Thr Leu Pro Asp Thr Pro Asn Glu Leu

65 70 75 80

gga gcg cca tct gct ttc gca gat gta ctc act ggt gcc cca tcc cga 288
Gly Ala Pro Ser Ala Phe Ala Asp Val Leu Thr Gly Ala Pro Ser Arg
85 90 95

gcc tca aag agt act aca tcc cga caa cag ctc gta aat tcg ttg ctt 336
Ala Ser Lys Ser Thr Thr Ser Arg Gln Gln Leu Val Asn Ser Leu Leu
100 105 110

gcc gcc aga gaa gcg ccc acc ggc ggt gaa aga cct cct aaa ttt acg 384
Ala Ala Arg Glu Ala Pro Thr Gly Gly Glu Arg Pro Pro Lys Phe Thr
115 120 125

aaa tta agt gac gag gaa ctc gaa gca ctc cgc gaa cat gtc gac cat 432
Lys Leu Ser Asp Glu Glu Leu Glu Ala Leu Arg Glu His Val Asp His
130 135 140

caa tcg aaa caa ctc gat agt caa aaa tct gag ctg gcc ggt gta cat 480
Gln Ser Lys Gln Leu Asp Ser Gln Lys Ser Glu Leu Ala Gly Val His
145 150 155 160

gct caa ctg ttt gag cag aag cag aga caa gaa caa gca ctc aac gtt 528
Ala Gln Leu Phe Glu Gln Lys Gln Arg Gln Glu Gln Ala Leu Asn Val
165 170 175

ctt gaa gtc gaa cgc gta gca gct ctc gaa aga gaa ctg aag aag cat 576
Leu Glu Val Glu Arg Val Ala Ala Leu Glu Arg Glu Leu Lys Lys His
180 185 190

caa caa gcc aac gag gct ttc caa aaa gct cta cgg gaa ata gga gag 624
Gln Gln Ala Asn Glu Ala Phe Gln Lys Ala Leu Arg Glu Ile Gly Glu
195 200 205

att gtc aca gct gta gct agg ggt gat ctc agt aag aag gta caa atc 672
Ile Val Thr Ala Val Ala Arg Gly Asp Leu Ser Lys Lys Val Gln Ile
210 215 220

cac tcc gtg gag atg gac cct gag att aca act ttc aag cgt gtt att 720
His Ser Val Glu Met Asp Pro Glu Ile Thr Thr Phe Lys Arg Val Ile
225 230 235 240

aat act atg atg gat caa ctt cag ata ttc tct agt gag gtt tct cgt 768
Asn Thr Met Met Asp Gln Leu Gln Ile Phe Ser Ser Glu Val Ser Arg
245 250 255

gta gct aga gag gtc ggc aca gaa ggt att ctc ggt gga caa gcc aag 816
Val Ala Arg Glu Val Gly Thr Glu Gly Ile Leu Gly Gly Gln Ala Lys
260 265 270

att tct ggt gtt gat ggt aca tgg aag gag ttg act gac aat gtc aac 864
Ile Ser Gly Val Asp Gly Thr Trp Lys Glu Leu Thr Asp Asn Val Asn

275 280 285

gtt atg gca caa aat ctc acc gat caa gtc cga gaa att gct tcc gtc 912
Val Met Ala Gln Asn Leu Thr Asp Gln Val Arg Glu Ile Ala Ser Val
290 295 300

act act gct gta gct cat gga gat ctc aca caa aag att gag aga cca 960
Thr Thr Ala Val Ala His Gly Asp Leu Thr Gln Lys Ile Glu Arg Pro
305 310 315 320

gcc cag ggt gag ata ctc caa ctg caa caa act atc aat acc atg gtg 1008
Ala Gln Gly Glu Ile Leu Gln Leu Gln Gln Thr Ile Asn Thr Met Val
325 330 335

gat caa ttg aga acg ttc gcc gcc gag gtc acc cgc gta gca aga gat 1056
Asp Gln Leu Arg Thr Phe Ala Ala Glu Val Thr Arg Val Ala Arg Asp
340 345 350

gta gga act gaa ggt att ctt ggg ggt caa gca gaa agc gaa ggc gtc 1104
Val Gly Thr Glu Gly Ile Leu Gly Gly Gln Ala Glu Ser Glu Gly Val
355 360 365

cag ggc atg tgg aac aca ttg ata gtg aac gtc aac gct atg gcc aat 1152
Gln Gly Met Trp Asn Thr Leu Ile Val Asn Val Asn Ala Met Ala Asn
370 375 380

aac ctc acc aca caa gtg cgc gat ata gcc att gtc aca aca gct gtc 1200
Asn Leu Thr Thr Gln Val Arg Asp Ile Ala Ile Val Thr Thr Ala Val
385 390 395 400

gca aag gga gac ctg act caa aag gtc caa gca gaa tgt aag ggt gaa 1248
Ala Lys Gly Asp Leu Thr Gln Lys Val Gln Ala Glu Cys Lys Gly Glu
405 410 415

atc aag cag ttg aag gag act ata aat tcc atg gtg gac caa tta caa 1296
Ile Lys Gln Leu Lys Glu Thr Ile Asn Ser Met Val Asp Gln Leu Gln
420 425 430

caa ttt gcg cga gaa gtc acg aag att gct agg gag gtc ggt acc gaa 1344
Gln Phe Ala Arg Glu Val Thr Lys Ile Ala Arg Glu Val Gly Thr Glu
435 440 445

ggt aga ctg ggt gga caa gca aca gtg cat gat gtt gaa ggc act tgg 1392
Gly Arg Leu Gly Gly Gln Ala Thr Val His Asp Val Glu Gly Thr Trp
450 455 460

aga gac ctc acc gaa aat gtg aat ggt atg gcc atg aat ctt acg aca 1440
Arg Asp Leu Thr Glu Asn Val Asn Gly Met Ala Met Asn Leu Thr Thr
465 470 475 480

caa gta cga gag att gca aag gtt acc acc gct gtc gcc aga gga gat 1488
Gln Val Arg Glu Ile Ala Lys Val Thr Thr Ala Val Ala Arg Gly Asp

485 490 495

ttg acc aag aag att gaa gtc gag gtt cag gga gaa atc gct tcg ctg 1536
Leu Thr Lys Lys Ile Glu Val Glu Val Gln Gly Glu Ile Ala Ser Leu
500 505 510

aaa gat acc atc aac acc atg gtg gac aga ctt agt aca ttc gct ttt 1584
Lys Asp Thr Ile Asn Thr Met Val Asp Arg Leu Ser Thr Phe Ala Phe
515 520 525

gag gtt agc aaa gtc gcc agg gag gtc gga act gat ggg act ctt ggt 1632
Glu Val Ser Lys Val Ala Arg Glu Val Gly Thr Asp Gly Thr Leu Gly
530 535 540

gga caa gcg caa gtt gat aac gtc gaa gga aag tgg aaa gac ctc act 1680
Gly Gln Ala Gln Val Asp Asn Val Glu Gly Lys Trp Lys Asp Leu Thr
545 550 555 560

gaa aat gtg aac acc atg gcc aga aac ttg act act caa gta cga ggt 1728
Glu Asn Val Asn Thr Met Ala Arg Asn Leu Thr Thr Gln Val Arg Gly
565 570 575

atc tcg act gtt aca caa gct att gcc aat gga gac atg agt cag aag 1776
Ile Ser Thr Val Thr Gln Ala Ile Ala Asn Gly Asp Met Ser Gln Lys
580 585 590

att gag gtt gct gct gcg ggt gaa ata ctc ata cta aag gaa acc ata 1824
Ile Glu Val Ala Ala Ala Gly Glu Ile Leu Ile Leu Lys Glu Thr Ile
595 600 605

aat aac atg gta gac aga ttg agt atc ttc tcc aac gaa gtg caa aga 1872
Asn Asn Met Val Asp Arg Leu Ser Ile Phe Ser Asn Glu Val Gln Arg
610 615 620

gtc gcc aaa gat gtg ggt gtg gat ggt aag atg ggt ggc caa gct gac 1920
Val Ala Lys Asp Val Gly Val Asp Gly Lys Met Gly Gly Gln Ala Asp
625 630 635 640

gtt gct ggg att ggc ggc cgt tgg aaa gag atc aca acg gat gtc aat 1968
Val Ala Gly Ile Gly Gly Arg Trp Lys Glu Ile Thr Thr Asp Val Asn
645 650 655

acc atg gct aac aac ttg aca acc caa gtg cgc gcc ttt ggt gat ata 2016
Thr Met Ala Asn Asn Leu Thr Thr Gln Val Arg Ala Phe Gly Asp Ile
660 665 670

act aac gcc gca acc gat ggc gac ttc aca aaa ttg atc act gtc gag 2064
Thr Asn Ala Ala Thr Asp Gly Asp Phe Thr Lys Leu Ile Thr Val Glu
675 680 685

gca tct gga gag atg gat gag ctg aag cga aag atc aac cag atg gtg 2112
Ala Ser Gly Glu Met Asp Glu Leu Lys Arg Lys Ile Asn Gln Met Val

690 695 700

tac aat ctg agg gac agt att caa aga aac acc ttg gct agg gag gct 2160
Tyr Asn Leu Arg Asp Ser Ile Gln Arg Asn Thr Leu Ala Arg Glu Ala
705 710 715 720

gcc gaa ttc gcc aat agg acg aag tct gaa ttc ttg gct aac atg tct 2208
Ala Glu Phe Ala Asn Arg Thr Lys Ser Glu Phe Leu Ala Asn Met Ser
725 730 735

cac gag att cga aca cct atg aac ggt atc att ggt atg act cag ttg 2256
His Glu Ile Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr Gln Leu
740 745 750

aca ctc gac acc gat ctt act caa tat caa cga gaa atg ctc aac att 2304
Thr Leu Asp Thr Asp Leu Thr Gln Tyr Gln Arg Glu Met Leu Asn Ile
755 760 765

gtt cac aac ttg gcc aac agt tta ttg acc atc att gat gat att ctc 2352
Val His Asn Leu Ala Asn Ser Leu Leu Thr Ile Ile Asp Asp Ile Leu
770 775 780

gat tta tca aag atc gaa gca aac cgt atg atc atg gag gag att cca 2400
Asp Leu Ser Lys Ile Glu Ala Asn Arg Met Ile Met Glu Glu Ile Pro
785 790 795 800

tac act ctt aga gga acc gtc ttc aac gcc ctc aag act ctc gct gtc 2448
Tyr Thr Leu Arg Gly Thr Val Phe Asn Ala Leu Lys Thr Leu Ala Val
805 810 815

aag gca aat gag aag ttc cta gac ctc act tac cgc gta gat agc tca 2496
Lys Ala Asn Glu Lys Phe Leu Asp Leu Thr Tyr Arg Val Asp Ser Ser
820 825 830

gtt cca gat cac gtg gtt ggt gat tca ttc cgt ctt cga caa gtt att 2544
Val Pro Asp His Val Val Gly Asp Ser Phe Arg Leu Arg Gln Val Ile
835 840 845

ctc aac ttg gtt gga aac gct atc aag ttc aca gag cat ggt gaa gtt 2592
Leu Asn Leu Val Gly Asn Ala Ile Lys Phe Thr Glu His Gly Glu Val
850 855 860

tcg ttg acc atc caa aaa gcc gag caa gat cat tgt gcg ccg aac gaa 2640
Ser Leu Thr Ile Gln Lys Ala Glu Gln Asp His Cys Ala Pro Asn Glu
865 870 875 880

tat gca gtc gag ttt tgt gtt tct gac act ggt atc ggt atc caa gct 2688
Tyr Ala Val Glu Phe Cys Val Ser Asp Thr Gly Ile Gly Ile Gln Ala
885 890 895

gat aag ctc aat ttg att ttc gac act ttc caa caa gct gac gga tct 2736
Asp Lys Leu Asn Leu Ile Phe Asp Thr Phe Gln Gln Ala Asp Gly Ser

900 905 910

atg acg agg aaa ttc gga ggt act ggt cta ggt cta tca att tcg aag 2784
Met Thr Arg Lys Phe Gly Gly Thr Gly Leu Gly Leu Ser Ile Ser Lys
915 920 925

aga ctt gta aac ctc atg cgt gga gat gtt tgg gtt aag agt cag tac 2832
Arg Leu Val Asn Leu Met Arg Gly Asp Val Trp Val Lys Ser Gln Tyr
930 935 940

gga aaa ggc agt tca ttc tac ttc acg tgt acc gtc cgc ctc gca acc 2880
Gly Lys Gly Ser Ser Phe Tyr Phe Thr Cys Thr Val Arg Leu Ala Thr
945 950 955 960

tca gat atc agt ttc att cag aaa caa ctc aag cca tat caa ggt cac 2928
Ser Asp Ile Ser Phe Ile Gln Lys Gln Leu Lys Pro Tyr Gln Gly His
965 970 975

aat gtt ttg ttt atc gac aaa gga cag act ggc cat ggc aaa gaa ata 2976
Asn Val Leu Phe Ile Asp Lys Gly Gln Thr Gly His Gly Lys Glu Ile
980 985 990

atc act atg ctt aca caa ctt ggt ttg gta ccc gtt gtt gtt gac tct 3024
Ile Thr Met Leu Thr Gln Leu Gly Leu Val Pro Val Val Val Asp Ser
995 1000 1005

gag cag cac act att ctt ctc ggc aat gga aga acc aag gag aag att 3072
Glu Gln His Thr Ile Leu Leu Gly Asn Gly Arg Thr Lys Glu Lys Ile
1010 1015 1020

gct tca act tat gac gtg att gtt gtg gac tca att gag tcc gct cga 3120
Ala Ser Thr Tyr Asp Val Ile Val Val Asp Ser Ile Glu Ser Ala Arg
1025 1030 1035 1040

aaa ctg cga tca atc gat gag ttc aag tat att cca att gtt ctc tta 3168
Lys Leu Arg Ser Ile Asp Glu Phe Lys Tyr Ile Pro Ile Val Leu Leu
1045 1050 1055

gct ccc gtt att cat gtc agc tta aag tct gct ttg gat ctt ggt atc 3216
Ala Pro Val Ile His Val Ser Leu Lys Ser Ala Leu Asp Leu Gly Ile
1060 1065 1070

act tct tac atg acc act cca tgt tta acg atc gat ctt ggc aat ggt 3264
Thr Ser Tyr Met Thr Thr Pro Cys Leu Thr Ile Asp Leu Gly Asn Gly
1075 1080 1085

atg att cct gct ttg gag aat cga gct gca ccc tca ttg gcg gac aac 3312
Met Ile Pro Ala Leu Glu Asn Arg Ala Ala Pro Ser Leu Ala Asp Asn
1090 1095 1100

aca aaa tcc ttc gac att ctc ttg gcc gaa gat aac atc gtc aat caa 3360
Thr Lys Ser Phe Asp Ile Leu Leu Ala Glu Asp Asn Ile Val Asn Gln

1105 1110 1115 1120

cgc tta gcg gtg aag att cta gaa aag tat cac cac gtc gtc aca gtc 3408
Arg Leu Ala Val Lys Ile Leu Glu Lys Tyr His His Val Val Thr Val
1125 1130 1135

gtt ggc aat ggt caa gaa gca cta gat gct atc aag gag aaa cga tac 3456
Val Gly Asn Gly Gln Glu Ala Leu Asp Ala Ile Lys Glu Lys Arg Tyr
1140 1145 1150

gat gtt att ctc atg gac gtt caa atg cca att atg gga gga ttc gaa 3504
Asp Val Ile Leu Met Asp Val Gln Met Pro Ile Met Gly Gly Phe Glu
1155 1160 1165

gca acc gct aag att aga gag tac gaa cgg agt ctt gga acg caa aga 3552
Ala Thr Ala Lys Ile Arg Glu Tyr Glu Arg Ser Leu Gly Thr Gln Arg
1170 1175 1180

acg cct att atc gca ctt aca gca cac gct atg ttg ggt gat cgc gaa 3600
Thr Pro Ile Ile Ala Leu Thr Ala His Ala Met Leu Gly Asp Arg Glu
1185 1190 1195 1200

aaa tgt att caa gcc caa atg gat gaa tat ctt tct aag cct ctg aaa 3648
Lys Cys Ile Gln Ala Gln Met Asp Glu Tyr Leu Ser Lys Pro Leu Lys
1205 1210 1215

caa aat cat ctt att cag acg atc ttg aaa tgt gca acc ctt gga ggt 3696
Gln Asn His Leu Ile Gln Thr Ile Leu Lys Cys Ala Thr Leu Gly Gly
1220 1225 1230

gca ttg ctc gag aag ggt agg gag gtt agg caa tcc gct aat gaa gag 3744
Ala Leu Leu Glu Lys Gly Arg Glu Val Arg Gln Ser Ala Asn Glu Glu
1235 1240 1245

agc ccc aat tcg caa aat ggt cct cgc ggt aca cag cat cct gca tca 3792
Ser Pro Asn Ser Gln Asn Gly Pro Arg Gly Thr Gln His Pro Ala Ser
1250 1255 1260

agt ccc aca cca gcc cat atg aga ccg gct atc gaa cct cgt gca tac 3840
Ser Pro Thr Pro Ala His Met Arg Pro Ala Ile Glu Pro Arg Ala Tyr
1265 1270 1275 1280

acg acc act ggc cct ata aat cat gga agt gca gag agt cct tca ctt 3888
Thr Thr Thr Gly Pro Ile Asn His Gly Ser Ala Glu Ser Pro Ser Leu
1285 1290 1295

gta acg gca gat gct gag gat cca ctt gcg agg ctt cta atg cgt gcg 3936
Val Thr Ala Asp Ala Glu Asp Pro Leu Ala Arg Leu Leu Met Arg Ala
1300 1305 1310

cat agc agc tag 3948
His Ser Ser

1315

<210> 15

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed oligonucleotide primer for PCR

<400> 15

ggtcaagcag aaagcgaagg cgtccagggc 30

<210> 16

<211> 1307

<212> PRT

<213> Magnapotrthe grisea

<400> 16

Met Ala Asp Ala Ala Thr Leu Ala Ala Val Ala Ala Ile Val Glu Asn
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Ile Ala Thr Asn Ser Gly Ala Pro Gly Lys Asn Ala Ser Phe Arg Ser
20 25 30

Ser Thr Tyr Val Gln Leu Pro Gly Pro Glu Ser Asp Glu Lys Lys Gln
35 40 45
Leu Glu Arg Glu Leu Ala Ala Leu Val Ile Arg Val Gln Gln Leu Glu
50 55 60
Thr Arg Ala Asn Ala Ala Pro Ala Thr Ile Phe Pro Asp Thr Pro Asn
65 70 75 80
Glu Thr Ala His Ser Leu Phe Gly Asp Asp Ser Ser Ser Pro Thr Ser
85 90 95
Ser Ser Ser Gly Arg Glu Pro Lys Arg Leu Lys Ser Ala Ser Ser Thr
100 105 110
Thr Arg Asn Gly Phe Thr Thr Asp Gly Arg Pro Ser Lys Leu Asn Ala
115 120 125
Ile Thr Asp Glu Glu Leu Glu Gly Leu Arg Glu His Val Asp Gly Gln
130 135 140
Ser Arg Leu Leu Asp Ser Gln Arg Ala Glu Leu Asp Gly Val Asn Ala
145 150 155 160
Gln Leu Leu Glu Gln Lys Gln Leu Gln Glu Arg Ala Leu Ala Ile Ile
165 170 175
Glu Gln Glu Arg Val Ala Thr Leu Glu Arg Glu Leu Trp Lys His Gln
180 185 190
Lys Ala Asn Glu Ala Phe Gln Lys Ala Leu Arg Glu Ile Gly Ser Ile
195 200 205
Val Thr Ala Ala Ala Arg Gly Asp Leu Ser Lys Arg Val Lys Ile Asn
210 215 220
Pro Ile Glu Met Asp Pro Glu Ile Thr Thr Phe Lys Arg Thr Met Asn
225 230 235 240

Ala Met Met Asp Gln Leu Gly Val Phe Ser Ser Glu Val Ser Arg Val
245 250 255

Ala Arg Glu Val Gly Thr Glu Gly Ile Leu Gly Gly Gln Ala Gln Ile
260 265 270

Glu Gly Val Asp Gly Thr Trp Lys Glu Leu Thr Asp Asn Val Asn Val
275 280 285

Met Ala Gln Asn Leu Thr Asp Gln Val Arg Glu Ile Ala Ser Val Thr
290 295 300

Thr Ala Val Ala His Gly Asp Leu Thr Gln Lys Ile Glu Ser Ala Ala
305 310 315 320

Lys Gly Glu Ile Leu Gln Leu Gln Gln Thr Ile Asn Thr Met Val Asp
325 330 335

Gln Leu Arg Thr Phe Ala Ser Glu Val Thr Arg Val Ala Arg Asp Val
340 345 350

Gly Thr Glu Gly Met Leu Gly Gly Gln Ala Asp Val Glu Gly Val Lys
355 360 365

Gly Met Trp Asn Glu Leu Thr Val Asn Val Asn Ala Met Ala Asn Asn
370 375 380

Leu Thr Thr Gln Val Arg Asp Ile Ile Asn Val Thr Thr Ala Val Ala
385 390 395 400

Lys Gly Asp Leu Thr Gln Lys Val Gln Ala Glu Cys Arg Gly Glu Ile
405 410 415

Phe Glu Leu Lys Asn Thr Ile Asn Ser Met Val Asp Gln Leu Gln Gln
420 425 430

Phe Ala Arg Glu Val Thr Lys Ile Ala Arg Glu Val Gly Thr Glu Gly
435 440 445

Arg Leu Gly Gly Gln Ala Thr Val His Asp Val Gln Gly Thr Trp Arg
450 455 460
Asp Leu Thr Glu Asn Val Asn Gly Met Ala Met Asn Leu Thr Thr Gln
465 470 475 480
Val Arg Glu Ile Ala Asn Val Thr Ser Ala Val Ala Ala Gly Asp Leu
485 490 495
Ser Lys Lys Ile Arg Val Glu Val Lys Gly Glu Ile Leu Asp Leu Lys
500 505 510
Asn Thr Ile Asn Thr Met Val Asp Arg Leu Gly Thr Phe Ala Phe Glu
515 520 525
Val Ser Lys Val Ala Arg Ala Val Gly Thr Asp Gly Thr Leu Gly Gly
530 535 540
Gln Ala Gln Val Glu Asn Val Glu Gly Lys Trp Lys Asp Leu Thr Glu
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Asn Val Asn Thr Met Ala Ser Asn Leu Thr Ser Gln Val Arg Gly Ile
565 570 575
Ser Thr Val Thr Gln Ala Ile Ala Asn Gly Asp Met Ser Arg Lys Ile
580 585 590
Asp Val Glu Ala Lys Gly Glu Ile Leu Ile Leu Lys Glu Thr Ile Asn
595 600 605
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Ala Lys Asp Val Gly Val Asp Gly Ile Met Gly Gly Gln Ala Asp Val
625 630 635 640
Ala Gly Leu Lys Gly Arg Trp Lys Glu Ile Thr Thr Asp Val Asn Thr
645 650 655

Met Ala Asn Asn Leu Thr Ala Gln Val Arg Ala Phe Gly Asp Ile Thr
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Asn Ala Ala Thr Asp Gly Asp Phe Thr Lys Leu Val Glu Val Glu Ala
675 680 685
Ser Gly Glu Met Asp Glu Leu Lys Arg Lys Ile Asn Gln Met Val Tyr
690 695 700
Asn Leu Arg Asp Ser Ile Gln Arg Asn Thr Gln Ala Arg Glu Ala Ala
705 710 715 720
Glu Leu Ala Asn Lys Thr Lys Ser Glu Phe Leu Ala Asn Met Ser His
725 730 735
Glu Ile Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr Gln Leu Thr
740 745 750
Leu Asp Thr Asp Leu Thr Gln Tyr Gln Arg Glu Met Leu Asn Ile Val
755 760 765
Asn Asn Leu Ala Met Ser Leu Leu Thr Ile Ile Asp Asp Ile Leu Asp
770 775 780
Leu Ser Lys Ile Glu Ala Lys Arg Met Val Ile Glu Glu Ile Pro Tyr
785 790 795 800
Thr Leu Arg Gly Thr Val Phe Asn Ala Leu Lys Thr Leu Ala Val Lys
805 810 815
Ala Asn Asp Lys Phe Leu Asp Leu Thr Tyr Arg Val Asp Ser Ser Val
820 825 830
Pro Asp His Val Ile Gly Asp Ser Phe Arg Leu Arg Gln Ile Ile Leu
835 840 845
Asn Leu Val Gly Asn Ala Ile Lys Phe Thr Glu His Gly Glu Val Ser
850 855 860

Leu Thr Ile Gln Lys Gly Asn Asp Val Thr Cys Leu Pro Asn Glu Tyr
865 870 875 880
Met Ile Glu Phe Val Val Ser Asp Thr Gly Ile Gly Ile Pro Thr Asp
885 890 895
Lys Leu Gly Leu Ile Phe Asp Thr Phe Gln Gln Ala Asp Gly Ser Met
900 905 910
Thr Arg Lys Phe Gly Gly Thr Gly Leu Gly Leu Ser Ile Ser Lys Arg
915 920 925
Leu Val Asn Leu Met Gly Gly Asp Val Trp Val Lys Ser Gln Tyr Gly
930 935 940
Lys Gly Ser Ser Phe Tyr Phe Thr Cys Arg Val Arg Leu Ala Asp Val
945 950 955 960
Asp Ile Ser Leu Ile Arg Lys Gln Leu Lys Pro Tyr Lys Gly His Gln
965 970 975
Val Leu Phe Ile Asp Lys Gly Lys Thr Gly His Gly Pro Glu Val Gly
980 985 990
Gln Met Leu Gly Gln Leu Gly Leu Val Pro Ile Val Leu Glu Ser Glu
995 1000 1005
Gln Asn His Thr Leu Thr Arg Val Arg Gly Lys Glu Cys Pro Tyr Asp
1010 1015 1020
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1025 1030 1035 1040
Asp Asp Phe Lys Tyr Leu Pro Ile Val Leu Leu Ala Pro Thr Val His
1045 1050 1055
Val Ser Leu Lys Ser Cys Leu Asp Leu Gly Ile Thr Ser Tyr Met Thr
1060 1065 1070

Met Pro Cys Lys Leu Ile Asp Leu Gly Asn Gly Met Val Pro Ala Leu
1075 1080 1085

Glu Asn Arg Ala Thr Pro Ser Leu Ser Asp Asn Thr Lys Ser Phe Glu
1090 1095 1100

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1105 1110 1115 1120

Ile Leu Glu Lys Tyr Asn His Val Val Thr Val Val Ser Asn Gly Ala
1125 1130 1135

Glu Ala Leu Glu Ala Val Lys Asp Asn Lys Tyr Asp Val Ile Leu Met
1140 1145 1150

Asp Val Gln Met Pro Val Met Gly Gly Phe Glu Ala Thr Ala Lys Ile
1155 1160 1165

Arg Glu Tyr Glu Arg Ser Leu Gly Thr Gln Arg Thr Pro Ile Ile Ala
1170 1175 1180

Leu Thr Ala His Ala Met Met Gly Asp Arg Glu Lys Cys Ile Glu Ala
1185 1190 1195 1200

Gln Met Asp Glu Tyr Leu Ser Lys Pro Leu Gln Gln Asn His Leu Ile
1205 1210 1215

Gln Thr Ile Leu Lys Cys Ala Thr Leu Gly Gly Ala Leu Leu Glu Gln
1220 1225 1230

Asn Arg Glu Arg Glu Leu Glu Leu Ala Arg His Ala Glu His Lys Gly
1235 1240 1245

Gly Leu Ser Thr Asp Pro Ala Arg Ala Ser Ser Val Met Arg Pro Pro
1250 1255 1260

Leu His His Arg Pro Val Thr Thr Ala Glu Ser Leu Ser Gly Gly Ala
1265 1270 1275 1280

Glu Ser Pro Ser Leu Met Ala Asn Asp Gly Glu Asp Pro Ile Gln Arg
1285 1290 1295

Ala Arg Ser Ser Leu Ser Glu Pro Gly Cys Leu
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<212> DNA

<213> Magnapotrthe grisea

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Ile Ala Thr Asn Ser Gly Ala Pro Gly Lys Asn Ala Ser Phe Arg Ser
20 25 30

agt acc tat gtc cag ctt ccc ggt ccg gaa tcc gac gag aag aaa cag 144
Ser Thr Tyr Val Gln Leu Pro Gly Pro Glu Ser Asp Glu Lys Lys Gln

35 40 45

ctc gag cgc gag ctt gcc gcc ctg gtg ata agg gta cag cag ctc gaa 192
Leu Glu Arg Glu Leu Ala Ala Leu Val Ile Arg Val Gln Gln Leu Glu
50 55 60

acc cgt gcc aac gcg gct cct gct aca ata ttc ccc gac aca ccc aac 240
Thr Arg Ala Asn Ala Ala Pro Ala Thr Ile Phe Pro Asp Thr Pro Asn
65 70 75 80

gaa act gca cat tca ctc ttt ggc gat gat agc tcg tcc cct acc agt 288
Glu Thr Ala His Ser Leu Phe Gly Asp Asp Ser Ser Ser Pro Thr Ser
85 90 95

tcg agc tca ggc cgg gag cct aaa cga ctg aag tcg gca tcc agc aca 336
Ser Ser Ser Gly Arg Glu Pro Lys Arg Leu Lys Ser Ala Ser Ser Thr
100 105 110

acg agg aat ggt ttc act acg gac ggt cgt cca tca aag ctc aac gca 384
Thr Arg Asn Gly Phe Thr Thr Asp Gly Arg Pro Ser Lys Leu Asn Ala
115 120 125

atc acc gat gag gag ctc gaa ggc ttg cgc gaa cat gtt gac ggc cag 432
Ile Thr Asp Glu Glu Leu Glu Gly Leu Arg Glu His Val Asp Gly Gln
130 135 140

tcc cgg ctg ctc gac agc caa agg gcc gag ctg gac ggc gtc aat gcc 480
Ser Arg Leu Leu Asp Ser Gln Arg Ala Glu Leu Asp Gly Val Asn Ala
145 150 155 160

caa ctc ttg gag cag aag cag ctg caa gag cgc gcc ctt gcc ata atc 528
Gln Leu Leu Glu Gln Lys Gln Leu Gln Glu Arg Ala Leu Ala Ile Ile
165 170 175

gag cag gaa cgt gta gcc act ttg gag aga gag cta tgg aaa cat caa 576
Glu Gln Glu Arg Val Ala Thr Leu Glu Arg Glu Leu Trp Lys His Gln
180 185 190

aag gcc aac gag gcc ttc cag aag gct ctc cgg gag att gga tcg ata 624
Lys Ala Asn Glu Ala Phe Gln Lys Ala Leu Arg Glu Ile Gly Ser Ile
195 200 205

gtg acc gct gca gcc cgg ggt gac ctc tct aag agg gtc aag ata aac 672
Val Thr Ala Ala Ala Arg Gly Asp Leu Ser Lys Arg Val Lys Ile Asn
210 215 220

ccg att gag atg gac cct gaa atc acc aca ttc aag agg acc atg aac 720
Pro Ile Glu Met Asp Pro Glu Ile Thr Thr Phe Lys Arg Thr Met Asn
225 230 235 240

gcc atg atg gat caa ctt ggc gtc ttc tct agt gaa gtc tcg cga gtg 768
Ala Met Met Asp Gln Leu Gly Val Phe Ser Ser Glu Val Ser Arg Val

245 250 255

gca aga gag gtc ggc acc gag ggc ata tta ggt gga cag gcc cag atc 816
Ala Arg Glu Val Gly Thr Glu Gly Ile Leu Gly Gly Gln Ala Gln Ile
260 265 270

gag gga gtg gac ggc acg tgg aaa gaa ctg acg gac aat gtc aac gtc 864
Glu Gly Val Asp Gly Thr Trp Lys Glu Leu Thr Asp Asn Val Asn Val
275 280 285

atg gcg cag aac ctg acc gac caa gtc cgc gaa atc gcc tca gtc act 912
Met Ala Gln Asn Leu Thr Asp Gln Val Arg Glu Ile Ala Ser Val Thr
290 295 300

aca gct gtg gcc cac gga gat ttg acc caa aag att gag agt gcg gcc 960
Thr Ala Val Ala His Gly Asp Leu Thr Gln Lys Ile Glu Ser Ala Ala
305 310 315 320

aag gga gaa atc cta cag ctt caa caa act ata aat acc atg gtg gac 1008
Lys Gly Glu Ile Leu Gln Leu Gln Gln Thr Ile Asn Thr Met Val Asp
325 330 335

caa cta cgc aca ttt gct tca gag gtt acc cgt gtc gcc cgt gac gtc 1056
Gln Leu Arg Thr Phe Ala Ser Glu Val Thr Arg Val Ala Arg Asp Val
340 345 350

gga acc gag gga atg ctc ggc ggg cag gct gac gtt gaa ggg gtc aag 1104
Gly Thr Glu Gly Met Leu Gly Gly Gln Ala Asp Val Glu Gly Val Lys
355 360 365

ggc atg tgg aat gag ctg acg gtc aac gtc aac gcc atg gcc aac aat 1152
Gly Met Trp Asn Glu Leu Thr Val Asn Val Asn Ala Met Ala Asn Asn
370 375 380

tta aca acc caa gtg cgc gac atc atc aac gtt acc aca gcc gtc gca 1200
Leu Thr Thr Gln Val Arg Asp Ile Ile Asn Val Thr Thr Ala Val Ala
385 390 395 400

aag gga gat ctt aca caa aag gtg cag gcg gaa tgt cgc ggc gag att 1248
Lys Gly Asp Leu Thr Gln Lys Val Gln Ala Glu Cys Arg Gly Glu Ile
405 410 415

ttt gag ctc aag aac acg atc aat tcc atg gtg gac cag ctg cag caa 1296
Phe Glu Leu Lys Asn Thr Ile Asn Ser Met Val Asp Gln Leu Gln Gln
420 425 430

ttt gct cgc gag gtt acc aag atc gcc aga gag gtt ggt acc gaa gga 1344
Phe Ala Arg Glu Val Thr Lys Ile Ala Arg Glu Val Gly Thr Glu Gly
435 440 445

cgg ctg ggc ggc caa gca act gtt cac gat gta cag gga act tgg cga 1392
Arg Leu Gly Gly Gln Ala Thr Val His Asp Val Gln Gly Thr Trp Arg

450 455 460

gat ctc aca gaa aac gtg aac gga atg gct atg aat ctc acc aca caa 1440
Asp Leu Thr Glu Asn Val Asn Gly Met Ala Met Asn Leu Thr Thr Gln
465 470 475 480

gta cga gag ata gcc aat gtt acc agt gcc gtc gct gca ggc gac cta 1488
Val Arg Glu Ile Ala Asn Val Thr Ser Ala Val Ala Ala Gly Asp Leu
485 490 495

tcc aag aag atc agg gta gag gtc aag ggc gag att ctg gac ctc aaa 1536
Ser Lys Lys Ile Arg Val Glu Val Lys Gly Glu Ile Leu Asp Leu Lys
500 505 510

aat acc atc aac acc atg gtt gac cgc ctc gga act ttc gcc ttc gaa 1584
Asn Thr Ile Asn Thr Met Val Asp Arg Leu Gly Thr Phe Ala Phe Glu
515 520 525

gtc agc aaa gta gcc cga gcc gtc ggc aca gat ggc act ctt ggt ggt 1632
Val Ser Lys Val Ala Arg Ala Val Gly Thr Asp Gly Thr Leu Gly Gly
530 535 540

cag gct caa gtt gag aat gtg gag ggc aaa tgg aaa gac ctc acc gaa 1680
Gln Ala Gln Val Glu Asn Val Glu Gly Lys Trp Lys Asp Leu Thr Glu
545 550 555 560

aac gtc aac acc atg gcg tca aac ctc act tct cag gtc agg gga ata 1728
Asn Val Asn Thr Met Ala Ser Asn Leu Thr Ser Gln Val Arg Gly Ile
565 570 575

tca acc gtg aca caa gcc atc gcg aac ggt gac atg agc cga aag atc 1776
Ser Thr Val Thr Gln Ala Ile Ala Asn Gly Asp Met Ser Arg Lys Ile
580 585 590

gac gtg gaa gcc aag ggc gag ata cta atc ctc aag gaa act atc aac 1824
Asp Val Glu Ala Lys Gly Glu Ile Leu Ile Leu Lys Glu Thr Ile Asn
595 600 605

aac atg gtt gat cgt ctg tcg ata ttc tgc aat gaa gta caa cga gtc 1872
Asn Met Val Asp Arg Leu Ser Ile Phe Cys Asn Glu Val Gln Arg Val
610 615 620

gca aaa gat gta ggc gtt gat ggc att atg ggg gga caa gcc gac gtt 1920
Ala Lys Asp Val Gly Val Asp Gly Ile Met Gly Gly Gln Ala Asp Val
625 630 635 640

gca ggt ctc aag ggg cga tgg aag gag att acc acc gat gtc aac acc 1968
Ala Gly Leu Lys Gly Arg Trp Lys Glu Ile Thr Thr Asp Val Asn Thr
645 650 655

atg gcc aac aat ctt acg gcg caa gta cgc gct ttc gga gat ata acc 2016
Met Ala Asn Asn Leu Thr Ala Gln Val Arg Ala Phe Gly Asp Ile Thr

660 665 670

aat gcc gct acc gac gga gac ttc acc aag ctg gtc gag gtt gag gcg 2064
Asn Ala Ala Thr Asp Gly Asp Phe Thr Lys Leu Val Glu Val Glu Ala
675 680 685

tcg ggc gaa atg gac gaa ctg aag cgc aag atc aat caa atg gtc tac 2112
Ser Gly Glu Met Asp Glu Leu Lys Arg Lys Ile Asn Gln Met Val Tyr
690 695 700

aat ctc cga gac agt atc caa aga aac acg caa gca aga gaa gcc gca 2160
Asn Leu Arg Asp Ser Ile Gln Arg Asn Thr Gln Ala Arg Glu Ala Ala
705 710 715 720

gaa ttg gcc aac aag acg aag tcg gag ttc ctc gct aac atg tcc cac 2208
Glu Leu Ala Asn Lys Thr Lys Ser Glu Phe Leu Ala Asn Met Ser His
725 730 735

gaa atc cgc aca ccc atg aac ggt atc atc ggc atg aca caa ctt act 2256
Glu Ile Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr Gln Leu Thr
740 745 750

ctt gat aca gat ttg acg caa tac caa cgc gaa atg ctc aac att gtc 2304
Leu Asp Thr Asp Leu Thr Gln Tyr Gln Arg Glu Met Leu Asn Ile Val
755 760 765

aac aat ctc gcc atg agt ctg ctc acc att atc gac gac atc ctc gat 2352
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770 775 780

ctg tca aag att gag gct aag cgg atg gtt atc gag gag att cca tac 2400
Leu Ser Lys Ile Glu Ala Lys Arg Met Val Ile Glu Glu Ile Pro Tyr
785 790 795 800

acg tta cga gga acg gtc ttc aac gca ctg aag act ttg gcg gtc aag 2448
Thr Leu Arg Gly Thr Val Phe Asn Ala Leu Lys Thr Leu Ala Val Lys
805 810 815

gcg aac gac aag ttt ttg gat ctc acg tac cgt gtg gac agc tca gtt 2496
Ala Asn Asp Lys Phe Leu Asp Leu Thr Tyr Arg Val Asp Ser Ser Val
820 825 830

cct gac cac gtc atc ggt gac tcg ttc cgt ctg cgc cag att atc ctg 2544
Pro Asp His Val Ile Gly Asp Ser Phe Arg Leu Arg Gln Ile Ile Leu
835 840 845

aac ctg gtt ggc aat gcc atc aaa ttc acc gag cat gga gag gtc agc 2592
Asn Leu Val Gly Asn Ala Ile Lys Phe Thr Glu His Gly Glu Val Ser
850 855 860

ctt act atc cag aag ggc aac gac gtg acg tgc ctg cca aac gag tac 2640
Leu Thr Ile Gln Lys Gly Asn Asp Val Thr Cys Leu Pro Asn Glu Tyr

865 870 875 880

atg atc gaa ttt gtc gtg tcg gac acg ggc ata gga att cca acg gac 2688
Met Ile Glu Phe Val Val Ser Asp Thr Gly Ile Gly Ile Pro Thr Asp
885 890 895

aaa ctg ggt ctc atc ttc gac aca ttc cag cag gct gat gga tcc atg 2736
Lys Leu Gly Leu Ile Phe Asp Thr Phe Gln Gln Ala Asp Gly Ser Met
900 905 910

aca cgc aag ttt ggc gga acc ggg ctt ggt ctg tct att tcc aag agg 2784
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915 920 925

ctc gtc aac ctc atg ggc ggt gac gtg tgg gtc aag tca caa tac ggc 2832
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930 935 940

aag ggc agc tcg ttc tac ttc act tgt cgt gtc cgc ctc gcc gac gtg 2880
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945 950 955 960

gat atc tca ctc atc agg aag cag ctg aag cct tac aag gga cac cag 2928
Asp Ile Ser Leu Ile Arg Lys Gln Leu Lys Pro Tyr Lys Gly His Gln
965 970 975

gtc ctg ttc atc gat aag ggc aag act gga cac ggg ccc gag gtg ggg 2976
Val Leu Phe Ile Asp Lys Gly Lys Thr Gly His Gly Pro Glu Val Gly
980 985 990

cag atg ctc ggc cag ctg ggt ttg gtg ccc atc gtg ctg gaa tcc gag 3024
Gln Met Leu Gly Gln Leu Gly Leu Val Pro Ile Val Leu Glu Ser Glu
995 1000 1005

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Gln Asn His Thr Leu Thr Arg Val Arg Gly Lys Glu Cys Pro Tyr Asp
1010 1015 1020

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1025 1030 1035 1040

gac gac ttc aag tat ctg ccc atc gtt ctc ctg gcg cca act gtc cac 3168
Asp Asp Phe Lys Tyr Leu Pro Ile Val Leu Leu Ala Pro Thr Val His
1045 1050 1055

gtc agc ctg aaa tcc tgc ttg gac ttg ggt att acc tcg tat atg acg 3216
Val Ser Leu Lys Ser Cys Leu Asp Leu Gly Ile Thr Ser Tyr Met Thr
1060 1065 1070

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Met Pro Cys Lys Leu Ile Asp Leu Gly Asn Gly Met Val Pro Ala Leu

1075 1080 1085

gag aac cgt gcc aca cca tca cta tca gac aac act aag tcg ttc gaa 3312
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1090 1095 1100

att ctg ctg gcc gag gac aac acc gtc aac cag cgc ctg gcc gtt aag 3360
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1105 1110 1115 1120

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1125 1130 1135

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1140 1145 1150

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1155 1160 1165

cgt gaa tac gag cgc agc ctg ggc aca cag agg aca cca atc atc gcg 3552
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1170 1175 1180

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1185 1190 1195 1200

cag atg gac gag tac ctg tcg aag cct ctg cag cag aac cac ttg ata 3648
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1205 1210 1215

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1220 1225 1230

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1235 1240 1245

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Gly Leu Ser Thr Asp Pro Ala Arg Ala Ser Ser Val Met Arg Pro Pro
1250 1255 1260

cta cac cac cga ccg gtg act aca gcc gag tcg ctt tct ggt ggc gcc 3840
Leu His His Arg Pro Val Thr Thr Ala Glu Ser Leu Ser Gly Gly Ala
1265 1270 1275 1280

gaa agc ccc tcg ttg atg gca aat gac ggc gaa gat cca ata caa agg 3888
Glu Ser Pro Ser Leu Met Ala Asn Asp Gly Glu Asp Pro Ile Gln Arg

1285 1290 1295

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1300 1305

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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Designed oligonucleotide primer for PCR

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<210> 19
<211> 34
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<223> Description of Artificial Sequence:Designed
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<400> 19
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<210> 20
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
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oligonucleotide primer for Sequencing

<400> 20
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<210> 21
<211> 25
<212> DNA
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<223> Description of Artificial Sequence:Designed
oligonucleotide primer for sequencing

<400> 21
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<210> 22
<211> 25
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<223> Description of Artificial Sequence:Designed
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<210> 23
<211> 25
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:Designed
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<210> 24
<211> 25
<212> DNA
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<210> 25
<211> 25
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<223> Description of Artificial Sequence:Designed oligonucleotide primer for sequencing

<400> 25

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<210> 26

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Designed oligonucleotide primer for sequencing

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<210> 27

<211> 25

<212> DNA

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<223> Description of Artificial Sequence:Designed oligonucleotide primer for sequencing

<400> 27

acagaggaca ccaatcatcg cgctt 25

<210> 28

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed oligonucleotide primer for sequencing

<400> 28

gttttcccag tcacgac 17

<210> 29

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Designed
oligonucleotide primer for sequencing

<400> 29
caggaaacag ctatgac 17

<210> 30
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : Designed
oligonucleotide primer for PCR

<400> 30
aacatgtccc acgarattcg macacc 26

<210> 31
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for PCR

<400> 31

cacgagattc gvacacccat gaaygg 26

<210> 32

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for PCR

<400> 32

aggccttcca aaaggctctv cggga 25

<210> 33

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for PCR

<400> 33

gagatggacc ctgaaatcac mac 23

<210> 34

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for PCR

<400> 34

cagatattct cyagygaagt ytckcg 26

<210> 35

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for PCR

<400> 35

atagcrttgc caacmaggtt magaataa 28

<210> 36

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for PCR

<400> 36

aacttgatgg crttkccaac maggtt 26

<210> 37

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed
oligonucleotide primer for PCR

<400> 37
ctctgtgaac ttgatrgcrt tkccaac 27

<210> 38
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : Designed
oligonucleotide primer for PCR

<400> 38
atacactttt cncggtcacc catcat 26

<210> 39
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for PCR

<400> 39

tccatctgbg cctggataca cttttc 26

<210> 40

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for PCR

<400> 40

ggcttvgava gatactcgtc catctg 26

<210> 41

<211> 1293

<212> PRT

<213> Fusarium oxysporum

<400> 41

Met Val Asp Asp Ala Ala Leu Ala Ala Ala Ala Ser Ile Val Ala Ser
1 5 10 15
Ile Ala Pro Asp Pro Arg Leu Pro Asn Ser Ile Pro Val Gly Val Ala
20 25 30
Ser Gln Val Gln Leu Pro Gly Pro Asp Thr Pro Ala Lys Arg Lys Leu
35 40 45
Glu Leu Glu Leu Gln Asn Leu Ala Leu Arg Val Gly Lys Leu Glu Ser
50 55 60
Gln Ala Ser Ala Thr Ser Pro Phe Pro Glu Thr Pro Asn Glu Val Ile
65 70 75 80
Asp Thr Leu Phe Gly Glu Glu Ala Gln Ala Val Ala Val Arg Pro Lys
85 90 95
Pro Lys Val Phe His Ala Gln Gly Ser Leu His Ser Pro His Leu Pro
100 105 110
Ser Tyr Gln Leu Thr Glu Glu Ala Leu Glu Gly Leu Arg Glu His Val
115 120 125
Asp Asp Gln Ser Lys Leu Leu Asp Ser Gln Arg Gln Glu Leu Ala Gly
130 135 140
Val Asn Ala Gln Leu Leu Glu Gln Lys Gln Leu Gln Glu Arg Ala Leu
145 150 155 160
Glu Ile Leu Glu Gln Glu Arg Ile Ala Thr Leu Glu Arg Glu Leu Trp
165 170 175
Lys His Gln Lys Ala Asn Glu Ala Phe Gln Lys Ala Leu Arg Glu Ile
180 185 190
Gly Glu Ile Val Thr Ala Val Ala Arg Gly Asp Leu Thr Met Lys Val
195 200 205

Arg Met Asn Thr Val Glu Met Asp Pro Glu Ile Thr Thr Phe Lys Arg
210 215 220
Thr Ile Asn Ala Met Met Asp Gln Leu Gln Ile Phe Ala Ser Glu Val
225 230 235 240
Ser Arg Val Ala Arg Glu Val Gly Thr Glu Gly Leu Leu Gly Gly Gln
245 250 255
Ala Arg Ile Gly Gly Val Asp Gly Thr Trp Lys Glu Leu Thr Asp Asn
260 265 270
Val Asn Val Met Ala Gln Asn Leu Thr Asp Gln Val Arg Glu Ile Ala
275 280 285
Ser Val Thr Thr Ala Val Ala His Gly Asp Leu Thr Lys Lys Ile Glu
290 295 300
Arg Pro Ala Arg Gly Glu Ile Leu Gln Leu Gln Gln Thr Ile Asn Thr
305 310 315 320
Met Val Asp Gln Leu Arg Thr Phe Ala Ser Glu Val Thr Arg Val Ala
325 330 335
Arg Asp Val Gly Thr Glu Gly Met Leu Gly Gly Gln Ala Asp Val Gly
340 345 350
Gly Val Gln Gly Met Trp Asn Asp Leu Thr Val Asn Val Asn Ala Met
355 360 365
Ala Asn Asn Leu Thr Thr Gln Val Arg Asp Ile Ile Lys Val Thr Thr
370 375 380
Ala Val Ala Lys Gly Asp Leu Thr Gln Lys Val Gln Ala Asp Cys Arg
385 390 395 400
Gly Glu Ile Phe Glu Leu Lys Ser Thr Ile Asn Ser Met Val Asp Gln
405 410 415

Leu Gln Gln Phe Ala Arg Glu Val Thr Lys Ile Ala Arg Glu Val Gly
420 425 430
Thr Glu Gly Arg Leu Gly Gly Gln Ala Thr Val His Asp Val Glu Gly
435 440 445
Thr Trp Arg Asp Leu Thr Glu Asn Val Asn Gly Met Ala Met Asn Leu
450 455 460
Thr Thr Gln Val Arg Glu Ile Ala Lys Val Thr Thr Ala Val Ala Lys
465 470 475 480
Gly Asp Leu Thr Lys Lys Ile Gly Val Glu Val Lys Gly Glu Ile Ala
485 490 495
Glu Leu Lys Asn Thr Ile Asn Gln Met Val Asp Arg Leu Gly Thr Phe
500 505 510
Ala Val Glu Val Ser Lys Val Ala Arg Glu Val Gly Thr Asp Gly Thr
515 520 525
Leu Gly Gly Gln Ala Gln Val Ala Asn Val Glu Gly Lys Trp Lys Asp
530 535 540
Leu Thr Glu Asn Val Asn Thr Met Ala Ser Asn Leu Thr Val Gln Val
545 550 555 560
Arg Ser Ile Ser Thr Val Thr Gln Ala Ile Ala Asn Gly Asp Met Ser
565 570 575
Gln Lys Ile Lys Val Glu Ala Asn Gly Glu Ile Gln Val Leu Lys Glu
580 585 590
Thr Ile Asn Asn Met Val Asp Arg Leu Ser Ser Phe Cys Tyr Glu Val
595 600 605
Gln Arg Val Ala Lys Asp Val Gly Val Asp Gly Lys Met Gly Ala Gln
610 615 620

Ala Asp Val Gly Gly Leu Asp Gly Arg Trp Lys Glu Ile Thr Thr Asp
625 630 635 640
Val Asn Thr Met Ala Ser Asn Leu Thr Thr Gln Val Arg Ala Phe Ser
645 650 655
Asp Ile Thr Asn Leu Ala Thr Asp Gly Asp Phe Thr Lys Leu Val Asp
660 665 670
Val Glu Ala Ser Gly Glu Met Asp Glu Leu Lys Arg Lys Ile Asn Gln
675 680 685
Met Ile Ser Asn Leu Arg Asp Ser Ile Gln Arg Asn Thr Gln Ala Arg
690 695 700
Glu Ala Ala Glu Leu Ala Asn Lys Thr Lys Ser Glu Phe Leu Ala Asn
705 710 715 720
Met Ser His Glu Ile Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr
725 730 735
Gln Leu Thr Leu Asp Thr Asp Leu Thr Gln Tyr Gln Arg Glu Met Leu
740 745 750
Asn Ile Val Asn Asn Leu Ala Asn Ser Leu Leu Thr Ile Ile Asp Asp
755 760 765
Ile Leu Asp Leu Ser Lys Ile Glu Ala Arg Arg Met Val Ile Glu Glu
770 775 780
Ile Pro Tyr Thr Leu Arg Gly Thr Val Phe Asn Ala Leu Lys Thr Leu
785 790 795 800
Ala Val Lys Ala Asn Glu Lys Phe Leu Asp Leu Thr Tyr Lys Val Asp
805 810 815
Ser Ser Val Pro Asp Tyr Val Ile Gly Asp Ser Phe Arg Leu Arg Gln
820 825 830

Ile Ile Leu Asn Leu Val Gly Asn Ala Ile Lys Phe Thr Glu His Gly
835 840 845

Glu Val Ser Leu Thr Ile Lys Glu Ser Met Gly Gln Asn Asn Val Arg
850 855 860

Pro Gly Glu Tyr Ala Val Glu Phe Val Val Glu Asp Thr Gly Ile Gly
865 870 875 880

Ile Ala Gln Asp Lys Leu Asp Leu Ile Phe Asp Thr Phe Gln Gln Ala
885 890 895

Asp Gly Ser Met Thr Arg Lys Phe Gly Gly Thr Gly Leu Gly Leu Ser
900 905 910

Ile Ser Lys Arg Leu Val Asn Leu Met Gly Gly Asp Leu Trp Val Asn
915 920 925

Ser Glu His Gly Lys Gly Ser Glu Phe His Phe Thr Cys Leu Val Lys
930 935 940

Leu Ala Pro Asp Asp Ala Ala Leu Ile Glu Gln Gln Ile Arg Pro Tyr
945 950 955 960

Arg Gly His Gln Val Leu Phe Val Asp Lys Ala Gln Ser Gln Asn Ala
965 970 975

Thr Ser Ile Lys Pro Met Leu Glu Lys Ile Gly Leu Lys Pro Val Val
980 985 990

Val Asp Ser Glu Lys Ser Pro Ala Leu Thr Arg Leu Gln Ser Gly Gly
995 1000 1005

Ser Leu Pro Tyr Asp Ala Ile Leu Val Asp Ser Ile Asp Thr Ala Arg
1010 1015 1020

Arg Leu Arg Ala Val Asp Asp Phe Lys Tyr Leu Pro Ile Val Leu Leu
1025 1030 1035 1040

Ala Pro Val Val His Val Ser Leu Lys Ser Cys Leu Asp Leu Gly Ile
1045 1050 1055

Thr Ser Tyr Met Thr Thr Pro Cys Lys Leu Ile Asp Leu Gly Asn Gly
1060 1065 1070

Met Ile Pro Ala Leu Glu Asn Arg Ala Thr Pro Ser Leu Ala Asp Asn
1075 1080 1085

Thr Lys Ser Phe Glu Ile Leu Leu Ala Glu Asp Asn Thr Val Asn Gln
1090 1095 1100

Arg Leu Ala Val Lys Ile Leu Glu Lys Tyr His His Val Val Thr Val
1105 1110 1115 1120

Val Gly Asn Gly Trp Glu Ala Val Lys Ala Val Gln Ser Lys Lys Phe
1125 1130 1135

Asp Val Ile Leu Met Asp Val Gln Met Pro Ile Met Gly Gly Phe Glu
1140 1145 1150

Ala Thr Gly Lys Ile Arg Glu Tyr Glu Arg Gly Ile Gly Ser His Arg
1155 1160 1165

Thr Pro Ile Ile Ala Leu Thr Ala His Ala Met Met Gly Asp Arg Glu
1170 1175 1180

Lys Cys Ile Gln Ala Gln Met Asp Glu Tyr Leu Ser Lys Pro Leu Gln
1185 1190 1195 1200

Gln Asn His Leu Ile Gln Thr Ile Leu Lys Cys Ala Thr Leu Gly Gly
1205 1210 1215

Pro Leu Leu Glu Lys Asn Arg Glu Arg Glu Leu Ala Leu His Ala Glu
1220 1225 1230

Thr Lys Ser Lys His Lys Glu Gly Gly Gln Gly Leu Leu Arg Pro Thr
1235 1240 1245

Leu Glu Ser Arg Ser Phe Thr Ser Arg Glu Pro Leu Leu Gly Asn Gly
1250 1255 1260
Lys Glu Ser Pro Ala Ile Leu Ala Thr Asp Glu Asp Pro Leu Ala Arg
1265 1270 1275 1280
Ala Arg Leu Asp Leu Ser Asp Met Arg Ser Leu Thr Asn
1285 1290

<210> 42
<211> 3882
<212> DNA
<213> Fusarium oxysporum

<220>
<221> CDS
<222> (1)..(3882)

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1 5 10 15

att gct cca gat ccc cgt ctg ccc aat tcg ata ccg gtt ggt gta gct 96
Ile Ala Pro Asp Pro Arg Leu Pro Asn Ser Ile Pro Val Gly Val Ala
20 25 30

tct cag gtg caa ctc cca ggg cca gat act ccc gcc aag cgc aag ctc 144
Ser Gln Val Gln Leu Pro Gly Pro Asp Thr Pro Ala Lys Arg Lys Leu
35 40 45

gaa ctc gag ctt cag aac ctt gct cta cgt gtt gga aag ctc gag agc 192
Glu Leu Glu Leu Gln Asn Leu Ala Leu Arg Val Gly Lys Leu Glu Ser
50 55 60

cag gcc tca gct acc tct cca ttc cca gaa acg ccc aac gag gtt att 240
Gln Ala Ser Ala Thr Ser Pro Phe Pro Glu Thr Pro Asn Glu Val Ile
65 70 75 80

gac act ctt ttt ggc gaa gag gct cag gct gtg gcg gtc cgt ccc aag 288
Asp Thr Leu Phe Gly Glu Glu Ala Gln Ala Val Ala Val Arg Pro Lys
85 90 95

cct aaa gtc ttt cac gcc caa ggt agc ctg cac tct ccg cat ctg cca 336
Pro Lys Val Phe His Ala Gln Gly Ser Leu His Ser Pro His Leu Pro
100 105 110

tct tat cag ctg acc gaa gaa gcc ctt gaa gga ctt cga gaa cat gtg 384
Ser Tyr Gln Leu Thr Glu Glu Ala Leu Glu Gly Leu Arg Glu His Val
115 120 125

gac gac caa tcc aag tta ctc gat agt cag cgc cag gag ctc gct ggt 432
Asp Asp Gln Ser Lys Leu Leu Asp Ser Gln Arg Gln Glu Leu Ala Gly

130 135 140

gta aat gct cag ctc ttg gag cag aag cag cta caa gag cga gcc ctc 480
Val Asn Ala Gln Leu Leu Glu Gln Lys Gln Leu Gln Glu Arg Ala Leu
145 150 155 160

gag atc ctc gag cag gaa cgt att gct act ctg gag cgc gag ctt tgg 528
Glu Ile Leu Glu Gln Glu Arg Ile Ala Thr Leu Glu Arg Glu Leu Trp
165 170 175

aag cat cag aaa gcc aac gag gct ttc caa aag gct cta cga gaa att 576
Lys His Gln Lys Ala Asn Glu Ala Phe Gln Lys Ala Leu Arg Glu Ile
180 185 190

gga gag att gtt aca gcc gtt gct cgc ggt gat ttg acc atg aag gtt 624
Gly Glu Ile Val Thr Ala Val Ala Arg Gly Asp Leu Thr Met Lys Val
195 200 205

cgc atg aac act gtt gaa atg gac cct gaa atc aca aca ttc aag cgc 672
Arg Met Asn Thr Val Glu Met Asp Pro Glu Ile Thr Thr Phe Lys Arg
210 215 220

act atc aac gct atg atg gac cag ctg caa ata ttt gct agc gaa gtc 720
Thr Ile Asn Ala Met Met Asp Gln Leu Gln Ile Phe Ala Ser Glu Val
225 230 235 240

tcg cga gtc gct cgt gaa gtc ggt acc gaa gga ttg ctt ggt ggc caa 768
Ser Arg Val Ala Arg Glu Val Gly Thr Glu Gly Leu Leu Gly Gly Gln
245 250 255

gcc cgt atc ggc ggc gtc gac gga aca tgg aag gaa ttg act gac aac 816
Ala Arg Ile Gly Gly Val Asp Gly Thr Trp Lys Glu Leu Thr Asp Asn
260 265 270

gta aac gtt atg gcc cag aat ctt act gat caa gtg agg gag ata gca 864
Val Asn Val Met Ala Gln Asn Leu Thr Asp Gln Val Arg Glu Ile Ala
275 280 285

tcg gtt acc acc gcc gtg gcc cac ggc gat ctg act aaa aag atc gaa 912
Ser Val Thr Thr Ala Val Ala His Gly Asp Leu Thr Lys Lys Ile Glu
290 295 300

cga cct gcc aga ggc gag ata ttg caa tta caa caa acg att aac acc 960
Arg Pro Ala Arg Gly Glu Ile Leu Gln Leu Gln Gln Thr Ile Asn Thr
305 310 315 320

atg gtg gac caa tta cga aca ttt gct tct gaa gtc aca cgt gta gcg 1008
Met Val Asp Gln Leu Arg Thr Phe Ala Ser Glu Val Thr Arg Val Ala
325 330 335

aga gat gtc ggg acc gaa ggc atg tta ggc ggg caa gcc gat gtt ggg 1056
Arg Asp Val Gly Thr Glu Gly Met Leu Gly Gly Gln Ala Asp Val Gly

340 345 350

gga gtg cag ggc atg tgg aac gat ctc acc gtc aat gtc aat gcc atg 1104
Gly Val Gln Gly Met Trp Asn Asp Leu Thr Val Asn Val Asn Ala Met
355 360 365

gcc aac aac ttg acg act caa gtg cgc gac att atc aag gtt acc aca 1152
Ala Asn Asn Leu Thr Thr Gln Val Arg Asp Ile Ile Lys Val Thr Thr
370 375 380

gct gtc gcc aag gga gat ctt aca caa aag gtc caa gcc gat tgc agg 1200
Ala Val Ala Lys Gly Asp Leu Thr Gln Lys Val Gln Ala Asp Cys Arg
385 390 395 400

gga gag ata ttc gag ctc aag tca acc atc aac tcc atg gtt gac cag 1248
Gly Glu Ile Phe Glu Leu Lys Ser Thr Ile Asn Ser Met Val Asp Gln
405 410 415

ctg caa cag ttc gcc cgc gag gtt acc aag att gcc cgt gaa gtc gga 1296
Leu Gln Gln Phe Ala Arg Glu Val Thr Lys Ile Ala Arg Glu Val Gly
420 425 430

acc gaa gga cgc ctg gga ggg cag gcc act gtg cat gat gtt gaa ggc 1344
Thr Glu Gly Arg Leu Gly Gly Gln Ala Thr Val His Asp Val Glu Gly
435 440 445

acc tgg agg gat ctg acg gag aac gtc aac ggc atg gcc atg aac ttg 1392
Thr Trp Arg Asp Leu Thr Glu Asn Val Asn Gly Met Ala Met Asn Leu
450 455 460

acc act caa gtg cga gaa att gcc aag gtt aca aca gct gtc gcc aaa 1440
Thr Thr Gln Val Arg Glu Ile Ala Lys Val Thr Thr Ala Val Ala Lys
465 470 475 480

ggt gac ttg aca aag aag att ggg gtt gag gtc aag ggt gaa att gca 1488
Gly Asp Leu Thr Lys Lys Ile Gly Val Glu Val Lys Gly Glu Ile Ala
485 490 495

gaa ctg aag aac acc att aac cag atg gtg gat cgt ctt ggt acg ttt 1536
Glu Leu Lys Asn Thr Ile Asn Gln Met Val Asp Arg Leu Gly Thr Phe
500 505 510

gcc gtt gag gtg agc aag gta gcc agg gaa gta ggc aca gat gga aca 1584
Ala Val Glu Val Ser Lys Val Ala Arg Glu Val Gly Thr Asp Gly Thr
515 520 525

ttg ggt gga cag gct caa gtt gcc aat gtt gaa ggt aaa tgg aag gat 1632
Leu Gly Gly Gln Ala Gln Val Ala Asn Val Glu Gly Lys Trp Lys Asp
530 535 540

ctc aca gaa aac gtc aac aca atg gcg tca aat ctc aca gtc cag gtc 1680
Leu Thr Glu Asn Val Asn Thr Met Ala Ser Asn Leu Thr Val Gln Val

545 550 555 560

cga agt atc tca aca gtt act caa gcc att gcg aac ggc gac atg agc 1728
Arg Ser Ile Ser Thr Val Thr Gln Ala Ile Ala Asn Gly Asp Met Ser
565 570 575

cag aag atc aag gtc gaa gca aat gga gag ata caa gtg ctg aaa gaa 1776
Gln Lys Ile Lys Val Glu Ala Asn Gly Glu Ile Gln Val Leu Lys Glu
580 585 590

acc atc aat aac atg gtt gac cgt ttg tct agc ttc tgt tac gaa gtg 1824
Thr Ile Asn Asn Met Val Asp Arg Leu Ser Ser Phe Cys Tyr Glu Val
595 600 605

cag cga gtt gcc aag gat gtg ggt gtt gat gga aag atg ggt gct caa 1872
Gln Arg Val Ala Lys Asp Val Gly Val Asp Gly Lys Met Gly Ala Gln
610 615 620

gcc gac gta ggt ggt cta gac ggc cgc tgg aaa gag atc acc aca gat 1920
Ala Asp Val Gly Gly Leu Asp Gly Arg Trp Lys Glu Ile Thr Thr Asp
625 630 635 640

gtc aac aca atg gct agt aac ctg act aca caa gtg cgc gcc ttc tca 1968
Val Asn Thr Met Ala Ser Asn Leu Thr Thr Gln Val Arg Ala Phe Ser
645 650 655

gat ata acc aac ttg gcc acc gac ggg gat ttc acc aag cta gtc gac 2016
Asp Ile Thr Asn Leu Ala Thr Asp Gly Asp Phe Thr Lys Leu Val Asp
660 665 670

gtc gaa gca tcg ggt gag atg gac gag ctc aag cgc aag atc aac cag 2064
Val Glu Ala Ser Gly Glu Met Asp Glu Leu Lys Arg Lys Ile Asn Gln
675 680 685

atg att tca aat ctg cgc gat tct att cag cgt aat act cag gcc agg 2112
Met Ile Ser Asn Leu Arg Asp Ser Ile Gln Arg Asn Thr Gln Ala Arg
690 695 700

gaa gct gcc gaa ctt gcc aac aag acc aag tca gag ttc ctc gcc aac 2160
Glu Ala Ala Glu Leu Ala Asn Lys Thr Lys Ser Glu Phe Leu Ala Asn
705 710 715 720

atg tcc cat gaa att cga acg ccg atg aac ggt atc atc gga atg act 2208
Met Ser His Glu Ile Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr
725 730 735

caa ctg aca ttg gac acc gat ctg act caa tat cag agg gag atg ctt 2256
Gln Leu Thr Leu Asp Thr Asp Leu Thr Gln Tyr Gln Arg Glu Met Leu
740 745 750

aac att gtc aat aat ctt gcc aat agc ctc ttg acg ata att gac gat 2304
Asn Ile Val Asn Asn Leu Ala Asn Ser Leu Leu Thr Ile Ile Asp Asp

755 760 765

atc ttg gat ctt tcc aag att gaa gct cgg aga atg gtc att gag gag 2352
Ile Leu Asp Leu Ser Lys Ile Glu Ala Arg Arg Met Val Ile Glu Glu
770 775 780

att cct tac aca ctg cgt gga acc gtc ttc aat gcc ctc aag act ctc 2400
Ile Pro Tyr Thr Leu Arg Gly Thr Val Phe Asn Ala Leu Lys Thr Leu
785 790 795 800

gct gtc aag gca aat gag aag ttc ttg gat ctc acc tac aag gtc gat 2448
Ala Val Lys Ala Asn Glu Lys Phe Leu Asp Leu Thr Tyr Lys Val Asp
805 810 815

agc tcc gtg cct gac tac gtt att ggc gac tcc ttc cgt ctc aga caa 2496
Ser Ser Val Pro Asp Tyr Val Ile Gly Asp Ser Phe Arg Leu Arg Gln
820 825 830

att atc ctc aac ctt gtt ggc aat gct atc aag ttc aca gag cat ggt 2544
Ile Ile Leu Asn Leu Val Gly Asn Ala Ile Lys Phe Thr Glu His Gly
835 840 845

gag gtc agc cta acg atc aag gag agc atg ggg caa aac aat gtc cga 2592
Glu Val Ser Leu Thr Ile Lys Glu Ser Met Gly Gln Asn Asn Val Arg
850 855 860

cct gga gag tat gcg gtt gag ttt gtc gtg gag gac acg ggc ata gga 2640
Pro Gly Glu Tyr Ala Val Glu Phe Val Val Glu Asp Thr Gly Ile Gly
865 870 875 880

atc gcc caa gat aaa ctg gat ttg atc ttc gac acg ttc caa caa gcg 2688
Ile Ala Gln Asp Lys Leu Asp Leu Ile Phe Asp Thr Phe Gln Gln Ala
885 890 895

gat ggt tcc atg acg cgc aag ttt ggc gga aca ggt cta ggt cta tct 2736
Asp Gly Ser Met Thr Arg Lys Phe Gly Gly Thr Gly Leu Gly Leu Ser
900 905 910

att tcg aaa cga ctc gtc aat ctc atg ggt ggt gat ctc tgg gta aac 2784
Ile Ser Lys Arg Leu Val Asn Leu Met Gly Gly Asp Leu Trp Val Asn
915 920 925

agt gaa cat ggc aag ggc agt gaa ttt cac ttc aca tgc tta gtc aag 2832
Ser Glu His Gly Lys Gly Ser Glu Phe His Phe Thr Cys Leu Val Lys
930 935 940

ctt gct cct gac gat gct gct ctg atc gag caa cag atc cgc ccc tac 2880
Leu Ala Pro Asp Asp Ala Ala Leu Ile Glu Gln Gln Ile Arg Pro Tyr
945 950 955 960

cga ggt cat caa gtg cta ttc gtc gac aag gcc cag tcg cag aac gcc 2928
Arg Gly His Gln Val Leu Phe Val Asp Lys Ala Gln Ser Gln Asn Ala

965 970 975

acc tca atc aag cct atg ctt gag aag atc ggg ctg aag cct gtc gtt 2976
Thr Ser Ile Lys Pro Met Leu Glu Lys Ile Gly Leu Lys Pro Val Val
980 985 990

gtg gat tcg gag aag agt cct gcg ctg act cgt ctt caa agc ggt ggc 3024
Val Asp Ser Glu Lys Ser Pro Ala Leu Thr Arg Leu Gln Ser Gly Gly
995 1000 1005

tcc ctt ccc tat gat gct atc ctc gtc gat tcc atc gac act gcg aga 3072
Ser Leu Pro Tyr Asp Ala Ile Leu Val Asp Ser Ile Asp Thr Ala Arg
1010 1015 1020

agg tta aga gcc gtg gac gat ttc aag tac ctt cct atc gtc ttg ctg 3120
Arg Leu Arg Ala Val Asp Asp Phe Lys Tyr Leu Pro Ile Val Leu Leu
1025 1030 1035 1040

gca cca gtt gtt cac gtt agt ctg aag tcg tgc ttg gat ctg gga att 3168
Ala Pro Val Val His Val Ser Leu Lys Ser Cys Leu Asp Leu Gly Ile
1045 1050 1055

acg tcg tat atg acc acg cca tgc aag ctc att gat cta gga aat ggc 3216
Thr Ser Tyr Met Thr Thr Pro Cys Lys Leu Ile Asp Leu Gly Asn Gly
1060 1065 1070

atg att ccg gct ctc gag aac cgg gcg aca cct tca ctc gct gac aac 3264
Met Ile Pro Ala Leu Glu Asn Arg Ala Thr Pro Ser Leu Ala Asp Asn
1075 1080 1085

acg aaa tct ttc gaa att ctg ctc gcc gaa gac aac acc gtc aac caa 3312
Thr Lys Ser Phe Glu Ile Leu Leu Ala Glu Asp Asn Thr Val Asn Gln
1090 1095 1100

cga tta gca gtg aaa att ctc gag aag tat cac cat gtg gta aca gtg 3360
Arg Leu Ala Val Lys Ile Leu Glu Lys Tyr His His Val Val Thr Val
1105 1110 1115 1120

gtt ggt aac ggc tgg gaa gct gtc aaa gcc gtc caa agc aag aaa ttc 3408
Val Gly Asn Gly Trp Glu Ala Val Lys Ala Val Gln Ser Lys Lys Phe
1125 1130 1135

gat gtc att ctt atg gat gta caa atg ccg atc atg gga ggc ttc gaa 3456
Asp Val Ile Leu Met Asp Val Gln Met Pro Ile Met Gly Gly Phe Glu
1140 1145 1150

gcc acg ggc aag att cga gaa tac gaa cgt ggc ata ggg agc cac cgc 3504
Ala Thr Gly Lys Ile Arg Glu Tyr Glu Arg Gly Ile Gly Ser His Arg
1155 1160 1165

aca ccc atc att gct cta acg gcc cac gcc atg atg ggt gac cga gag 3552
Thr Pro Ile Ile Ala Leu Thr Ala His Ala Met Met Gly Asp Arg Glu

1170 1175 1180

aag tgt atc caa gct cag atg gac gag tat ttg tcc aaa ccc ttg cag 3600
Lys Cys Ile Gln Ala Gln Met Asp Glu Tyr Leu Ser Lys Pro Leu Gln
1185 1190 1195 1200

caa aac cat ctc atc cag acg atc ctc aaa tgc gcg acg ctc ggc ggc 3648
Gln Asn His Leu Ile Gln Thr Ile Leu Lys Cys Ala Thr Leu Gly Gly
1205 1210 1215

cct ttg ctt gaa aag aat cgt gaa cgg gaa ctg gca ctt cat gcc gag 3696
Pro Leu Leu Glu Lys Asn Arg Glu Arg Glu Leu Ala Leu His Ala Glu
1220 1225 1230

acg aaa tcg aag cac aag gag ggg gga cag ggt ctg cta cga ccc aca 3744
Thr Lys Ser Lys His Lys Glu Gly Gly Gln Gly Leu Leu Arg Pro Thr
1235 1240 1245

ctc gag agc cgc tca ttc aca agt cga gaa cct ctg ttg gga aat ggc 3792
Leu Glu Ser Arg Ser Phe Thr Ser Arg Glu Pro Leu Leu Gly Asn Gly
1250 1255 1260

aag gag agc cct gcc att ctg gct act gat gag gat ccc ctg gca aga 3840
Lys Glu Ser Pro Ala Ile Leu Ala Thr Asp Glu Asp Pro Leu Ala Arg
1265 1270 1275 1280

gca cgt ctt gac ctc tct gat atg cga agt ctt acc aac taa 3882
Ala Arg Leu Asp Leu Ser Asp Met Arg Ser Leu Thr Asn
1285 1290

<210> 43
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : Designed oligonucleotide primer for PCR

<400> 43
tcagatcgcc gtgggccacg gcggtggta 29

<210> 44
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence : Designed oligonucleotide primer for PCR

<400> 44

cgacaaggcc cagtcgcaga acgccacc 28

<210> 45

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for DNA sequencing

<400> 45

aagtttggcg gaacaggtct aggtctatc 29

<210> 46

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for DNA sequencing

<400> 46

tgccagcaag acgataggaa ggtacttga 29

<210> 47

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for DNA sequencing

<400> 47

cctcaccatg ctctgtgaac ttgatagc 28

<210> 48

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for DNA sequencing

<400> 48

gccattgtgt tgacatctgt ggtgatctc 29

<210> 49

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for DNA sequencing

<400> 49

gatgcttcca aagctcgcgc tccagagtag 30

<210> 50

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for DNA sequencing

<400> 50

ccgaagacaa caccgtcaac caacgattag 30

<210> 51

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for DNA sequencing

<400> 51

ggaccctgaa atcacaacat tcaagcgc 28

<210> 52

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for PCR

<400> 52

tgcactagta tggttgacga cgcggccctc gc 32

<210> 53

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for PCR

<400> 53

gagctgcagt tagttggtaa gacttcgcat atc 33

<210> 54

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for DNA sequencing

<400> 54

gtaaaacgac ggccag 16

<210> 55

<211> 1307

<212> PRT

<213> Mycospharella tritici

<400> 55

Met Leu Gln Glu Glu Thr Ser Ala Ala Val Ala Ser Ile Leu Ser Asn
1 5 10 15

Phe Ala Lys Gln Tyr Ala Pro Leu Glu Ala Asp Ser Phe Pro Ala Lys
20 25 30

Ala Ile Ala Asn Gly Ile Lys Asn Thr Lys Ile Ala Leu Pro Gly Asp
35 40 45

Asp Ser Val Glu Lys Arg Thr Leu Glu Arg Glu Leu Thr Ser Leu Ala
50 55 60

Thr Arg Ile Gln Phe Leu Glu Ala Arg Ala Thr Ser Gly Thr Ser Ser
65 70 75 80

Leu Pro Ile Thr Pro Asn Glu Pro Leu Ser Ser Ala Phe Ser Glu Asp
85 90 95

Thr Ser Ser Pro Arg Ser Ala Ala Asn Gln His Arg Gln Arg Ser Ser
100 105 110

Ser Trp Val Asn Asn Leu Leu Ala Lys Ser Glu Gly Glu Pro His Pro

115 120 125

Arg Gln Leu Thr Glu Glu Gln Phe Ser Phe Leu Arg Glu His Ile Asp

130 135 140

Gln Gln Ala Gln Glu Ile Arg Thr Gln Lys Glu Phe Ile Asp Gly Ile

145 150 155 160

Lys Ser Gln Leu Thr His Gln Gln Thr Ala Thr Lys Ala Ala Leu Asp

165 170 175

Thr Leu Gly Asn Ser Gln Ser Ile Glu Gln Leu Lys Arg Glu Ile Glu

180 185 190

Lys Asn Ala Gln Ile Asn Ala Thr Tyr Gln Lys Val Leu Arg Glu Ile

195 200 205

Gly Thr Ile Ile Thr Ala Val Ala Asn Gly Asp Leu Ser Lys Lys Val

210 215 220

Leu Ile His Ala Thr Glu Lys Asp Pro Glu Ile Ala Arg Phe Lys His

225 230 235 240

Thr Ile Asn Lys Met Val Asp Gln Leu Gln Glu Phe Ala Ser Gln Val

245 250 255

Thr His Leu Ala Lys Glu Val Gly Thr Glu Gly Arg Leu Gly Gly Gln

260 265 270

Ala Val Val Pro Gly Val Asp Gly Ile Trp Ala Glu Leu Thr Gln Asn

275 280 285

Val Asn Val Met Ala Gln Asn Leu Thr Asp Gln Val Arg Glu Ile Ala

290 295 300

Val Val Thr Thr Ala Val Ala Gln Gly Asp Leu Ser Arg Lys Ile Gln

305 310 315 320

Arg Pro Ala Arg Gly Glu Ile Leu Gln Leu Gln Gln Thr Ile Asn Ser

325 330 335

Met Val Gly Gln Leu Arg Thr Phe Ala Thr Glu Val Thr Arg Val Ser

340 345 350

Arg Asp Val Gly Thr Glu Gly Val Leu Gly Gly Gln Ala Gln Ile Glu

355 360 365

Gly Val Gln Gly Met Trp Ser Asp Leu Thr Val Asn Val Asn Ala Met

370 375 380

Ala Asn Asn Leu Thr Ala Gln Val Arg Asp Ile Ala Glu Val Thr Thr

385 390 395 400

Ala Val Ala Arg Gly Asp Leu Thr Gln Gln Val Lys Ala Gln Cys Lys

405 410 415

Gly Glu Ile Leu Ala Leu Lys Thr Thr Ile Asn Ser Met Val His Gln

420 425 430

Leu Arg Gln Phe Ala His Glu Val Thr Lys Ile Ala Arg Glu Val Gly

435 440 445

Thr Glu Gly Arg Leu Gly Gly Gln Ala Thr Val His Gly Val Glu Gly

450 455 460

Thr Trp Lys Asp Leu Thr Glu Asn Val Asn Gly Met Ala Met Asn Leu

465 470 475 480

Thr Thr Gln Val Arg Glu Ile Ala Glu Val Thr Thr Ala Val Ala Gln

485 490 495

Gly Asp Leu Ser Lys Lys Val Glu Ala Glu Val Lys Gly Glu Ile Leu

500 505 510

Ala Leu Lys Ser Thr Ile Asn Ser Met Val Asp Arg Leu Gly Thr Phe

515 520 525

Ala Phe Glu Val Ser Lys Val Ala Arg Glu Val Gly Thr Glu Gly Val

530 535 540

Leu Gly Gly Gln Ala Glu Val Ala Asn Val Glu Gly Lys Trp Lys Asp
545 550 555 560

Leu Thr Asp Asn Val Asn Thr Met Ala Asn Asn Leu Thr Gly Gln Val
565 570 575

Arg Ser Ile Ser Asp Val Thr Gln Ala Ile Ala Arg Gly Asp Met Ser
580 585 590

Gln Arg Ile Lys Val His Ala Gln Gly Glu Ile Gln Thr Leu Lys Asp
595 600 605

Thr Ile Asn Asp Met Val Thr Arg Leu Asp Ala Trp Ser Leu Ala Val
610 615 620

Lys Arg Val Ala Arg Asp Val Gly Val Asp Gly Lys Met Gly Gly Gln
625 630 635 640

Ala Glu Val Glu Gly Ile Thr Gly Arg Trp Lys Glu Ile Thr Thr Asp
645 650 655

Val Asn Ile Met Ala Gln Asn Leu Thr Ser Gln Val Arg Ala Phe Ala
660 665 670

Asp Ile Thr His Ala Ala Met Lys Gly Asp Phe Thr Lys Met Ile Asn
675 680 685

Val Glu Ala Ser Gly Glu Met Asn Glu Leu Lys Asn Lys Ile Asn Lys
690 695 700

Met Val Leu Asn Leu Arg Glu Ser Ile Gln Lys Asn Asn Gln Ala Arg
705 710 715 720

Glu Ala Ala Glu Leu Ala Asn Lys Thr Lys Ser Glu Phe Leu Ala Asn
725 730 735

Met Ser His Glu Ile Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr

740 745 750

Gln Leu Thr Leu Asp Thr Glu Leu Glu Gln Asn Gln Arg Asp Met Leu

755 760 765

Asn Ile Val Phe Ser Leu Ala Asn Ser Leu Leu Thr Ile Ile Asp Asp

770 775 780

Ile Leu Asp Ile Ser Lys Ile Glu Ala Asn Arg Met Ile Leu Glu Glu

785 790 795 800

Glu Pro Phe Ser Leu Arg Gly Leu Val Phe Asn Ser Leu Lys Ser Leu

805 810 815

Ala Val Arg Ala Asn Glu Lys Asp Ile Ser Leu Val Tyr Asp Thr Asp

820 825 830

Ser Ser Val Pro Asp Tyr Ile Val Gly Asp Ser Phe Arg Leu Arg Gln

835 840 845

Ile Ile Leu Asn Leu Ala Gly Asn Ala Ile Lys Phe Thr Glu His Gly

850 855 860

Glu Val Arg Val Lys Ile Phe Ser Asp His Ser Thr Arg Cys Thr Asp

865 870 875 880

Ser Glu Val Val Val Lys Phe Ala Val Ser Asp Thr Gly Ile Gly Ile

885 890 895

His Ser Asn Lys Leu Asp Leu Ile Phe Asp Thr Phe Gln Gln Ala Asp

900 905 910

Gly Ser Thr Thr Arg Lys Phe Gly Gly Thr Gly Leu Gly Leu Ser Ile

915 920 925

Ser Arg Arg Leu Val Thr Leu Met Arg Gly Lys Met Trp Val Glu Ser

930 935 940

Asn Tyr Gly Ser Gly Ser Thr Phe Phe Phe Thr Xaa Val Val Arg Leu

945 950 955 960

Gly Asn Pro Asp Val Ala Lys Ile Met Pro Gln Leu Gln Gln Tyr Arg

965 970 975

Lys His Asn Val Leu Phe Val Asp Asn Gly Asn Thr Asp Ser Ser Glu

980 985 990

Glu Ile Ala Ala Gly Ile Arg Ala Leu Asp Leu Val Pro Cys Val Val

995 1000 1005

Gly Lys Gly Lys Val Pro His Ser Glu Ile Ser Pro Asp Asp Gln Tyr

1010 1015 1020

Asp Cys Val Ile Ile Asp Asn Ser Glu Thr Ala Gln Lys Leu Arg Ser

1025 1030 1035 1040

Leu Glu Arg Phe Lys Tyr Ile Pro Ile Val Met Val Ala Pro Ala Ile

1045 1050 1055

Ser Val Asn Phe Lys Thr Ala Leu Glu Asn Gly Ile Ser Ser Tyr Met

1060 1065 1070

Thr Thr Pro Cys Leu Pro Ile Asp Leu Gly Asn Ala Leu Val Pro Ala

1075 1080 1085

Leu Glu Gly Arg Ala Ala Pro Met Ser Ala Asp His Ser Arg Thr Phe

1090 1095 1100

Asp Ile Leu Leu Ala Glu Asp Asn Ala Val Asn Gln Lys Leu Ala Val

1105 1110 1115 1120

Lys Ile Leu Thr Lys His Asn His Thr Val Thr Val Ala Asn Asn Gly

1125 1130 1135

Leu Glu Ala Phe Glu Ala Ile Arg Lys Lys Arg Phe Asp Val Val Leu

1140 1145 1150

Met Asp Val Gln Met Pro Val Met Gly Gly Phe Glu Ala Thr Ala Lys

1155 1160 1165

Ile Arg Glu Tyr Glu Arg Thr His Glu Leu Ala Arg Ser Pro Ile Ile

1170 1175 1180

Ala Leu Thr Ala His Ala Met Leu Gly Asp Arg Glu Lys Cys Ile Gln

1185 1190 1195 1200

Ala Gln Met Asp Glu Tyr Leu Ser Lys Pro Leu Lys Xaa Asn Gln Leu

1205 1210 1215

Ile Gln Thr Ile Leu Lys Cys Ala Thr Leu Gly Gly Ala Leu Leu Asp

1220 1225 1230

Arg Arg Asn Asp Gly Arg Gly Leu Leu Met Glu Glu Asp Lys Pro Val

1235 1240 1245

Ser Asp Asn Ser Ser Leu Pro Ala Asp His Asn Arg Leu Leu Thr Pro

1250 1255 1260

Pro Lys Arg Pro Gly Val Asp Arg Gly Tyr Thr Glu Asn Gly Pro Pro

1265 1270 1275 1280

Gly Leu Glu Ser Pro Ala Ile Val Thr Asp Asp Gln Asp Asp Pro Met

1285 1290 1295

Ile Arg Glu Ser Leu Val Arg Ala His Ser Ser

1300 1305

<210> 56

<211> 3924

<212> DNA

<213> Mycospharella tritici

<220>

<221> CDS

<222> (1)..(3924)

<400> 56

atg ctg caa gaa gag act tcg gca gct gtg gcc agc atc ctc tcc aac 48
Met Leu Gln Glu Glu Thr Ser Ala Ala Val Ala Ser Ile Leu Ser Asn
1 5 10 15

ttc gcc aag cag tat gct cct ctg gaa gcg gat tca ttc cct gca aag 96
Phe Ala Lys Gln Tyr Ala Pro Leu Glu Ala Asp Ser Phe Pro Ala Lys
20 25 30

gcc atc gcg aat gga att aag aac acc aaa att gct cta ccg ggc gat 144
Ala Ile Ala Asn Gly Ile Lys Asn Thr Lys Ile Ala Leu Pro Gly Asp
35 40 45

gat tca gtg gag aag cgt act cta gag cgc gag ctg act agc ctt gcg 192
Asp Ser Val Glu Lys Arg Thr Leu Glu Arg Glu Leu Thr Ser Leu Ala
50 55 60

acg cgg atc cag ttt ctc gag gct cgc gct aca agc gga acc agt tcg 240
Thr Arg Ile Gln Phe Leu Glu Ala Arg Ala Thr Ser Gly Thr Ser Ser
65 70 75 80

tta ccc atc act ccc aac gag cca ctt tct tcg gca ttc tcg gag gac 288

Leu Pro Ile Thr Pro Asn Glu Pro Leu Ser Ser Ala Phe Ser Glu Asp
85 90 95

acc tcg tcg cca agg tcc gca gcg aac cag cac cgc cag cgc tca tcg 336
Thr Ser Ser Pro Arg Ser Ala Ala Asn Gln His Arg Gln Arg Ser Ser
100 105 110

tca tgg gtc aac aac ctc ctg gct aag agc gag ggc gag cct cat cct 384
Ser Trp Val Asn Asn Leu Leu Ala Lys Ser Glu Gly Glu Pro His Pro
115 120 125

cga caa ctc act gaa gaa caa ttt tca ttt cta cgt gag cac atc gac 432
Arg Gln Leu Thr Glu Glu Gln Phe Ser Phe Leu Arg Glu His Ile Asp
130 135 140

caa caa gcg caa gag att cgg act cag aag gaa ttt atc gac ggt atc 480
Gln Gln Ala Gln Glu Ile Arg Thr Gln Lys Glu Phe Ile Asp Gly Ile
145 150 155 160

aaa tcg cag ctg acg cac cag caa acc gct aca aaa gct gca ctc gat 528
Lys Ser Gln Leu Thr His Gln Gln Thr Ala Thr Lys Ala Ala Leu Asp
165 170 175

acc ttg ggc aac tcg cag tca atc gag cag ctg aag cgg gag att gag 576
Thr Leu Gly Asn Ser Gln Ser Ile Glu Gln Leu Lys Arg Glu Ile Glu
180 185 190

aaa aat gcg caa atc aat gct aca tac caa aaa gtg ctg cga gag atc 624
Lys Asn Ala Gln Ile Asn Ala Thr Tyr Gln Lys Val Leu Arg Glu Ile
195 200 205

ggc acc atc att aca gct gtc gcc aat gga gat ctc agc aag aaa gtg 672
Gly Thr Ile Ile Thr Ala Val Ala Asn Gly Asp Leu Ser Lys Lys Val
210 215 220

ctc att cat gcc acg gag aaa gat ccg gag att gcg agg ttc aag cac 720
Leu Ile His Ala Thr Glu Lys Asp Pro Glu Ile Ala Arg Phe Lys His
225 230 235 240

acg atc aac aag atg gtg gac cag ttg caa gag ttt gct agt caa gta 768
Thr Ile Asn Lys Met Val Asp Gln Leu Gln Glu Phe Ala Ser Gln Val
245 250 255

aca cat ttg gcg aaa gag gtg gga aca gaa gga cgc ctc gga gga caa 816
Thr His Leu Ala Lys Glu Val Gly Thr Glu Gly Arg Leu Gly Gly Gln
260 265 270

gcc gtc gtg cct ggc gtc gac ggt att tgg gcg gag ctt acg caa aac 864
Ala Val Val Pro Gly Val Asp Gly Ile Trp Ala Glu Leu Thr Gln Asn
275 280 285

gtg aac gtc atg gcc caa aat ttg acc gac cag gtg cga gaa atc gca 912

Val Asn Val Met Ala Gln Asn Leu Thr Asp Gln Val Arg Glu Ile Ala
290 295 300

gtt gta acc acc gcc gtt gca caa ggt gat ctg agc cgc aag att caa 960
Val Val Thr Thr Ala Val Ala Gln Gly Asp Leu Ser Arg Lys Ile Gln
305 310 315 320

cga cca gcc aga ggc gag att ctc caa ctt caa cag act atc aac tcc 1008
Arg Pro Ala Arg Gly Glu Ile Leu Gln Leu Gln Gln Thr Ile Asn Ser
325 330 335

atg gtg gga cag ctc cgg acc ttc gca acg gaa gtt acg aga gtg tcg 1056
Met Val Gly Gln Leu Arg Thr Phe Ala Thr Glu Val Thr Arg Val Ser
340 345 350

cgc gat gtc ggc acg gag ggt gtt ctt gga ggt caa gct caa atc gaa 1104
Arg Asp Val Gly Thr Glu Gly Val Leu Gly Gly Gln Ala Gln Ile Glu
355 360 365

ggc gta cag ggc atg tgg agc gac ctt act gtg aac gtg aat gct atg 1152
Gly Val Gln Gly Met Trp Ser Asp Leu Thr Val Asn Val Asn Ala Met
370 375 380

gca aac aat ctc act gcc cag gtg cga gat att gcg gag gtg aca aca 1200
Ala Asn Asn Leu Thr Ala Gln Val Arg Asp Ile Ala Glu Val Thr Thr
385 390 395 400

gcc gtg gcc cga ggc gac ctc acg cag cag gtt aaa gcg caa tgt aag 1248
Ala Val Ala Arg Gly Asp Leu Thr Gln Gln Val Lys Ala Gln Cys Lys
405 410 415

ggg gag atc ctg gcc ttg aaa acc acc atc aac tcc atg gtg cac cag 1296
Gly Glu Ile Leu Ala Leu Lys Thr Thr Ile Asn Ser Met Val His Gln
420 425 430

cta cgg caa ttc gcg cat gaa gtc acc aag atc gcg cgt gag gtc ggg 1344
Leu Arg Gln Phe Ala His Glu Val Thr Lys Ile Ala Arg Glu Val Gly
435 440 445

aca gaa ggt cgc cta ggt gga caa gca aca gtt cac gga gtc gag ggc 1392
Thr Glu Gly Arg Leu Gly Gly Gln Ala Thr Val His Gly Val Glu Gly
450 455 460

aca tgg aaa gac ttg acg gag aac gta aat ggc atg gcc atg aat ctg 1440
Thr Trp Lys Asp Leu Thr Glu Asn Val Asn Gly Met Ala Met Asn Leu
465 470 475 480

acc acc caa gtg cgc gag atc gca gaa gtc aca acc gcc gtc gcg caa 1488
Thr Thr Gln Val Arg Glu Ile Ala Glu Val Thr Thr Ala Val Ala Gln
485 490 495

gga gat ctc agc aaa aag gtc gag gcc gaa gtc aag ggt gaa att ttg 1536

Gly Asp Leu Ser Lys Lys Val Glu Ala Glu Val Lys Gly Glu Ile Leu
500 505 510

gcc ttg aag agc acc atc aat tcc atg gtt gac cgt ctg ggt acg ttt 1584
Ala Leu Lys Ser Thr Ile Asn Ser Met Val Asp Arg Leu Gly Thr Phe
515 520 525

gct ttc gag gtt agc aag gtc gcg aga gaa gtc gga acc gaa gga gtt 1632
Ala Phe Glu Val Ser Lys Val Ala Arg Glu Val Gly Thr Glu Gly Val
530 535 540

ttg ggc gga caa gca gag gtt gcc aat gtc gaa gga aaa tgg aaa gat 1680
Leu Gly Gly Gln Ala Glu Val Ala Asn Val Glu Gly Lys Trp Lys Asp
545 550 555 560

ctt acc gac aat gtc aac acc atg gcc aac aac ttg act ggt cag gtg 1728
Leu Thr Asp Asn Val Asn Thr Met Ala Asn Asn Leu Thr Gly Gln Val
565 570 575

cgg agc att tca gac gtc aca cag gcc att gca cgc ggt gac atg agc 1776
Arg Ser Ile Ser Asp Val Thr Gln Ala Ile Ala Arg Gly Asp Met Ser
580 585 590

cag cga atc aag gtg cac gct cag gga gag att cag aca ttg aag gac 1824
Gln Arg Ile Lys Val His Ala Gln Gly Glu Ile Gln Thr Leu Lys Asp
595 600 605

acg atc aac gac atg gtg acg cga ctg gac gct tgg tca ctc gcg gtg 1872
Thr Ile Asn Asp Met Val Thr Arg Leu Asp Ala Trp Ser Leu Ala Val
610 615 620

aag cgg gtg gct cgt gac gtc ggt gtc gac ggc aag atg ggt gga cag 1920
Lys Arg Val Ala Arg Asp Val Gly Val Asp Gly Lys Met Gly Gly Gln
625 630 635 640

gca gaa gtc gaa ggc atc act ggt cgc tgg aag gag atc acg acc gat 1968
Ala Glu Val Glu Gly Ile Thr Gly Arg Trp Lys Glu Ile Thr Thr Asp
645 650 655

gtg aac att atg gct caa aat ttg acc tcg caa gtg aga gct ttt gcc 2016
Val Asn Ile Met Ala Gln Asn Leu Thr Ser Gln Val Arg Ala Phe Ala
660 665 670

gac att acc cac gcg gcc atg aaa gga gat ttc acc aag atg atc aat 2064
Asp Ile Thr His Ala Ala Met Lys Gly Asp Phe Thr Lys Met Ile Asn
675 680 685

gtc gaa gcg tct ggc gaa atg aac gag ctg aag aac aag atc aac aag 2112
Val Glu Ala Ser Gly Glu Met Asn Glu Leu Lys Asn Lys Ile Asn Lys
690 695 700

atg gtc ctc aac ttg cgc gaa agt atc cag aag aac aat caa gca aga 2160

Met Val Leu Asn Leu Arg Glu Ser Ile Gln Lys Asn Asn Gln Ala Arg
705 710 715 720

gag gcc gcc gag ttg gcc aac aag acg aaa tcg gag ttc ctg gca aac 2208
Glu Ala Ala Glu Leu Ala Asn Lys Thr Lys Ser Glu Phe Leu Ala Asn
725 730 735

atg tcc cac gag att cga aca cct atg aac gga atc atc gga atg aca 2256
Met Ser His Glu Ile Arg Thr Pro Met Asn Gly Ile Ile Gly Met Thr
740 745 750

cag ctt acc ttg gac acc gag ctt gag cag aac caa cgg gac atg ctc 2304
Gln Leu Thr Leu Asp Thr Glu Leu Glu Gln Asn Gln Arg Asp Met Leu
755 760 765

aac atc gtc ttc tcg ctc gcc aac agc tta ctg acg att att gat gac 2352
Asn Ile Val Phe Ser Leu Ala Asn Ser Leu Leu Thr Ile Ile Asp Asp
770 775 780

atc ttg gac att tcc aag att gaa gca aat cgc atg atc cta gag gaa 2400
Ile Leu Asp Ile Ser Lys Ile Glu Ala Asn Arg Met Ile Leu Glu Glu
785 790 795 800

gag ccg ttc tca ctg cga ggt ctc gtc ttc aac agc tta aag tca ctt 2448
Glu Pro Phe Ser Leu Arg Gly Leu Val Phe Asn Ser Leu Lys Ser Leu
805 810 815

gca gtc cga gcc aac gag aag gac atc agc ttg gtg tat gat acc gac 2496
Ala Val Arg Ala Asn Glu Lys Asp Ile Ser Leu Val Tyr Asp Thr Asp
820 825 830

agc tca gtg ccc gac tac atc gtg ggc gac tcc ttc cga ctt cga cag 2544
Ser Ser Val Pro Asp Tyr Ile Val Gly Asp Ser Phe Arg Leu Arg Gln
835 840 845

atc att ctc aat ctc gcc ggc aac gcc atc aaa ttc acc gag cac ggg 2592
Ile Ile Leu Asn Leu Ala Gly Asn Ala Ile Lys Phe Thr Glu His Gly
850 855 860

gaa gtg cgt gtt aag ata ttc tct gac cac agt aca cga tgc acc gat 2640
Glu Val Arg Val Lys Ile Phe Ser Asp His Ser Thr Arg Cys Thr Asp
865 870 875 880

agt gag gtt gtc gtc aaa ttc gcc gtc tcc gat act ggt att ggc atc 2688
Ser Glu Val Val Val Lys Phe Ala Val Ser Asp Thr Gly Ile Gly Ile
885 890 895

cac tcc aac aag ttg gat ttg atc ttc gac acg ttt cag cag gct gac 2736
His Ser Asn Lys Leu Asp Leu Ile Phe Asp Thr Phe Gln Gln Ala Asp
900 905 910

ggg tcg acc aca cgg aag ttc gga ggt act gga ttg ggc ctg tcg atc 2784

Gly Ser Thr Thr Arg Lys Phe Gly Gly Thr Gly Leu Gly Leu Ser Ile
915 920 925

tct cgg aga ctg gtg act ttg atg cgt ggc aag atg tgg gtc gaa tca 2832
Ser Arg Arg Leu Val Thr Leu Met Arg Gly Lys Met Trp Val Glu Ser
930 935 940

aat tat ggc tca ggc agc aca ttc ttc ttc acc tgk gtt gta cgg ctg 2880
Asn Tyr Gly Ser Gly Ser Thr Phe Phe Phe Thr Xaa Val Val Arg Leu
945 950 955 960

ggc aat ccg gat gtt gca aaa atc atg cca caa cta cag cag tat cga 2928
Gly Asn Pro Asp Val Ala Lys Ile Met Pro Gln Leu Gln Gln Tyr Arg
965 970 975

aag cac aac gtg ctc ttt gtc gac aac ggt aat acg gac agt tcg gag 2976
Lys His Asn Val Leu Phe Val Asp Asn Gly Asn Thr Asp Ser Ser Glu
980 985 990

gag atc gcg gct ggc atc cga gct ttg gat ctg gtc cct tgt gtg gtg 3024
Glu Ile Ala Ala Gly Ile Arg Ala Leu Asp Leu Val Pro Cys Val Val
995 1000 1005

ggc aag gga aag gtt cct cac tcc gaa atc agc cca gac gac cag tac 3072
Gly Lys Gly Lys Val Pro His Ser Glu Ile Ser Pro Asp Asp Gln Tyr

1010 1015 1020

gac tgc gtg atc atc gat aac agc gag acg gct cag aag ttg cgc agc 3120
Asp Cys Val Ile Ile Asp Asn Ser Glu Thr Ala Gln Lys Leu Arg Ser
1025 1030 1035 1040

ttg gaa cgt ttc aag tac att ccc atc gtc atg gtg gcg ccg gcc atc 3168
Leu Glu Arg Phe Lys Tyr Ile Pro Ile Val Met Val Ala Pro Ala Ile
1045 1050 1055

tcg gtg aac ttc aag acc gcg ttg gag aac gga atc tca agc tac atg 3216
Ser Val Asn Phe Lys Thr Ala Leu Glu Asn Gly Ile Ser Ser Tyr Met
1060 1065 1070

act acg cca tgc ctt cca atc gac ctg ggc aat gct ctg gtg ccc gca 3264
Thr Thr Pro Cys Leu Pro Ile Asp Leu Gly Asn Ala Leu Val Pro Ala
1075 1080 1085

ctc gag ggc cgc gca gca ccc atg tca gcc gac cac agt cgg aca ttc 3312
Leu Glu Gly Arg Ala Ala Pro Met Ser Ala Asp His Ser Arg Thr Phe
1090 1095 1100

gat atc ctc ctc gca gaa gac aac gcg gtg aat caa aaa ctc gcc gtc 3360
Asp Ile Leu Leu Ala Glu Asp Asn Ala Val Asn Gln Lys Leu Ala Val
1105 1110 1115 1120

aag atc ctg acc aag cac aac cac aca gtg aca gtc gcc aac aac ggc 3408
Lys Ile Leu Thr Lys His Asn His Thr Val Thr Val Ala Asn Asn Gly
1125 1130 1135

ctt gaa gcc ttt gaa gcg att cgc aag aag cgc ttc gat gtc gtt ctc 3456
Leu Glu Ala Phe Glu Ala Ile Arg Lys Lys Arg Phe Asp Val Val Leu
1140 1145 1150

atg gac gtg caa atg ccc gtc atg gga ggg ttc gaa gcg acg gcc aag 3504
Met Asp Val Gln Met Pro Val Met Gly Gly Phe Glu Ala Thr Ala Lys
1155 1160 1165

att cgc gaa tac gaa cga act cac gag cta gca cgt tcg ccc att atc 3552
Ile Arg Glu Tyr Glu Arg Thr His Glu Leu Ala Arg Ser Pro Ile Ile
1170 1175 1180

gcc ctc acc gca cac gcc atg ctt ggc gac cgc gag aag tgt atc caa 3600
Ala Leu Thr Ala His Ala Met Leu Gly Asp Arg Glu Lys Cys Ile Gln
1185 1190 1195 1200

gcg caa atg gac gag tat ctc tcc aaa ccc ctc aag ycc aat cag ctc 3648
Ala Gln Met Asp Glu Tyr Leu Ser Lys Pro Leu Lys Xaa Asn Gln Leu
1205 1210 1215

att cag acg atc ctg aaa tgt gcg acc cta ggc ggt gcg tta ctt gac 3696
Ile Gln Thr Ile Leu Lys Cys Ala Thr Leu Gly Gly Ala Leu Leu Asp

1220 1225 1230

cgg agg aac gat ggg cgc ggt ttg ctc atg gaa gag gac aaa ccc gtt 3744
Arg Arg Asn Asp Gly Arg Gly Leu Leu Met Glu Glu Asp Lys Pro Val
1235 1240 1245

tct gat aat tcg agt ctt cct gca gat cac aat cgg ttg ctc acg ccc 3792
Ser Asp Asn Ser Ser Leu Pro Ala Asp His Asn Arg Leu Leu Thr Pro
1250 1255 1260

ccg aaa cga ccg ggt gtc gat cgt ggg tac acg gag aat gga ccg ccc 3840
Pro Lys Arg Pro Gly Val Asp Arg Gly Tyr Thr Glu Asn Gly Pro Pro
1265 1270 1275 1280

ggt ttg gaa agt ccg gcg ata gta acc gac gac cag gat gat ccg atg 3888
Gly Leu Glu Ser Pro Ala Ile Val Thr Asp Asp Gln Asp Asp Pro Met
1285 1290 1295

atc aga gag agt ctt gtt cgt gcc cat agc agc tga 3924
Ile Arg Glu Ser Leu Val Arg Ala His Ser Ser
1300 1305

<210> 57
<211> 28
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for PCR

<400> 57

cggaaggagt cgcccacgat gtagtcgg 28

<210> 58

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for PCR

<400> 58

catggtggcg ccggccatct cggtgaac 28

<210> 59

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for DNA sequencing

<400> 59

tcgccagacg cttcgacatt gatcatcttg 30

<210> 60

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for DNA sequencing

<400> 60

ttcatggcca tgccatttac gttctccgtc 30

<210> 61

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for DNA sequencing

<400> 61

tacaagcgga accagttcgt tacccatcac 30

<210> 62

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for DNA sequencing

<400> 62

gactccttcc gacttcgaca gatcattctc 30

<210> 63

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for DNA sequencing

<400> 63

tccgtgtggt cgacccgtca gcctgctg 28

<210> 64

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for PCR

<400> 64

cccactagta tgctgcaaga agagacttcg 30

<210> 65

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for PCR

<400> 65

cctaagcttc tcagctgcta tgggcacgaa 30

<210> 66

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for DNA sequencing

<400> 66

caggaaacag ctatgaccat gattacgcca 30

<210> 67

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Designed oligonucleotide primer for DNA sequencing

<400> 67

tgtaaaacga cggccagtga attgtaatac 30

<210> 68

<211> 1438

<212> PRT

<213> Thanatephorus cucumeris

<400> 68

Met Ala Gly Thr Thr Gly Gly His Pro Phe Thr Ala His Leu Val Ala
1 5 10 15

Val Leu Ser Ile Tyr Glu Leu Gly Pro Gly Arg Pro Val Arg Ala Leu
20 25 30

Pro Thr Arg Ser Ser His Ser His Ser Ser Ser Gly Ser Arg His Ala
35 40 45

Arg Ala Leu Ser Val Pro Pro Phe Pro Pro Pro Pro Pro Met Ser Pro
50 55 60

Pro Asn Ala Pro Ile Asp Tyr Val Gly Ala Ala Pro Leu Pro Arg Tyr
65 70 75 80

Asp Gly Pro Arg Asp Trp Gln Thr Asp Ala Val Glu Arg Ala Leu Gly
85 90 95
Arg Val Ala Ala Arg Met Tyr Ala Ala Glu Ala Gln Leu Gln Asp Leu
100 105 110
Leu Ser Arg Glu Ser Ser Thr Ser Thr Pro Asp Pro Ala Leu Ser Pro
115 120 125
Arg Ser Asn Gly Leu Lys Lys Arg Arg Glu Asn Pro Gly Thr Pro Asp
130 135 140
Glu Arg Asp Pro Trp Gln Thr Val Arg Phe Gln Glu Val Gly Asp Gln
145 150 155 160
Asp Met Asp Pro Glu Pro Asp Thr Pro Val Ala Arg Pro Lys Asp Lys
165 170 175
Val Lys Pro Gly Thr Ile Asp Leu Ser Thr Leu Ser Gln Pro Thr Pro
180 185 190
Leu Ser Lys Val Ala Thr Asp Asn Pro Val Leu Pro Lys Pro Gly Pro
195 200 205
Arg Ser Ala Pro Thr Ser Ser Val Gly Ser Ile Met Pro Pro Phe Thr
210 215 220
Cys His Ser Cys Gly Arg Pro Met Gln Gly Pro Ala Ala Pro Asp Val
225 230 235 240
Ile His Ala Pro Gly Pro Leu Asp Val Val Thr Pro Ala Leu Gly Met
245 250 255
Gly Leu Gly Leu Ser Asp His Gly Ala Ala Glu Leu Arg Gln Lys Leu
260 265 270
Gly Phe Gly Asp His Glu Asp Asp Thr Gly Ser Pro Leu Val Leu Pro
275 280 285

Pro Gly Pro Leu Ser Ala Ala Ala Phe Glu Ser Ala Pro Gly Met Ser
290 295 300
Ala Val Glu Glu Leu Lys Leu Leu Lys Ala Gln Val Gln Asp Val Ala
305 310 315 320
Arg Val Cys Lys Ala Val Ala Glu Gly Asp Leu Ser Gln Lys Ile Thr
325 330 335
Val Pro Val Gln Gly Pro Val Met Val Gln Leu Lys Asp Val Ile Asn
340 345 350
Thr Met Val Asp Lys Leu Gly Arg Phe Ala Gln Glu Val Thr Arg Val
355 360 365
Ser Leu Glu Val Gly Thr Glu Gly Arg Leu Gly Gly Gln Ala Ile Val
370 375 380
Arg Asp Val Arg Gly Thr Trp Ser Glu Leu Thr Thr Val Val Asn Arg
385 390 395 400
Leu Ala Ala Asn Leu Thr Ser Gln Val Arg Gly Ile Ala Glu Val Thr
405 410 415
Lys Ala Val Ala Lys Gly Asp Leu Ser Lys Gln Ile Gly Val Asp Ala
420 425 430
Lys Gly Glu Ile Leu Glu Leu Lys Asn Thr Val Asn Thr Met Val Val
435 440 445
Arg Leu Arg Met Phe Ala Gly Glu Val Thr Arg Val Ala Leu Asp Val
450 455 460
Gly Ser Arg Gly Ile Leu Gly Gly Gln Ala Tyr Val Pro Asp Val Glu
465 470 475 480
Gly Val Trp Gln Glu Leu Thr Asp Asn Val Asn Arg Met Cys Ser Asn
485 490 495

Leu Thr Asn Gln Val Arg Ser Ile Ala Leu Val Thr Thr Ala Val Ala
500 505 510
Glu Gly Asp Leu Thr Arg Lys Ile Glu Ile Glu Val Glu Gly Glu Met
515 520 525
Leu Thr Leu Lys Asn Thr Val Asn Ser Met Val Asp Gln Leu Ser Thr
530 535 540
Phe Ala Ser Glu Val Thr Arg Val Ala Leu Glu Val Gly Ser Met Gly
545 550 555 560
Ile Leu Gly Gly Gln Ala Gln Val Glu Gly Val Lys Gly Thr Trp Ala
565 570 575
Asp Leu Thr Arg Asn Val Asn Asn Met Ala Ser Asn Leu Thr Asn Gln
580 585 590
Val Arg Ser Ile Ala Lys Val Thr Thr Ala Val Ala His Gly Asp Leu
595 600 605
Arg Gln Phe Val Glu Val Asp Val Gln Gly Glu Met Leu Met Leu Lys
610 615 620
Asn Thr Val Asn Ser Met Val Ala Gln Leu Asp Thr Leu Ala Ser Glu
625 630 635 640
Val Ser Arg Val Ala Leu Glu Val Gly Ile Glu Gly Arg Leu Gly Gly
645 650 655
Gln Ala Val Val Gln Gly Val Glu Gly Val Trp Lys Val Leu Thr Asp
660 665 670
Asn Val Asn Leu Met Ala Leu Asn Leu Thr Thr Gln Val Arg Ser Ile
675 680 685
Ala Ala Val Thr Thr Ala Val Ala Arg Gly Asp Leu Ser Lys Asn Ile
690 695 700

Asp Val Asp Val Lys Gly Glu Ile Leu Asp Leu Lys Ile Thr Val Asn
705 710 715 720
Arg Met Thr Asp Ser Leu Arg Ile Phe Ala Ala Glu Val Thr Arg Val
725 730 735
Ala Arg Glu Val Gly Thr Leu Gly Arg Leu Gly Gly Gln Ala Phe Val
740 745 750
Pro Gly Val Ala Gly Val Trp Lys Asp Leu Thr Asp Asn Val Asn Val
755 760 765
Met Ala Ala Asn Leu Thr Leu Gln Val Arg Ala Ile Ala Arg Val Thr
770 775 780
Thr Ala Val Ser Val Gly Asp Leu Thr Thr Lys Val Glu Gly Ile Asp
785 790 795 800
Val Ala Gly Glu Ile Leu Asp Leu Val Asn Thr Ile Asn Gly Met Val
805 810 815
Asp Gln Leu Ala Val Phe Ala Ala Glu Val Thr Arg Val Ala Arg Glu
820 825 830
Val Gly Thr Glu Gly Arg Leu Gly Val Gln Ala Arg Val Glu Gly Met
835 840 845
Gln Gly Ser Trp Gln Ala Ile Thr Val Ser Val Asn Thr Met Ala Ala
850 855 860
Asn Leu Thr Ser Gln Val Arg Gly Phe Ala Gln Ile Ser Ala Ala Ala
865 870 875 880
Thr Asp Gly Asp Phe Thr Arg Phe Ile Thr Val Glu Ala Ser Gly Glu
885 890 895
Met Asp Ser Leu Lys Thr Gln Ile Asn Gln Met Val Tyr Asn Leu Arg
900 905 910

Glu Ser Ile Gln Arg Asn Thr Ala Ala Arg Glu Ala Ala Glu Leu Ala
915 920 925
Asn Arg Ser Lys Ser Glu Phe Leu Ala Asn Met Ser His Glu Ile Arg
930 935 940
Thr Pro Met Asn Gly Ile Ile Gly Met Thr Asp Leu Thr Leu Asp Thr
945 950 955 960
Glu Leu Thr Arg Thr Gln Lys Glu Asn Leu Leu Leu Val His Gln Leu
965 970 975
Ala Lys Ser Leu Leu Leu Ile Ile Asp Asp Ile Leu Asp Ile Ser Lys
980 985 990
Ile Glu Ala Gly Arg Met Thr Met Glu Gln Val Thr Tyr Ser Leu Arg
995 1000 1005
Gly Thr Ala Phe Gly Ile Leu Lys Thr Leu Val Val Arg Ala His Gln
1010 1015 1020
Gln Asn Leu Asn Leu Phe Tyr Glu Val Asp Pro Glu Ile Pro Asp Gln
1025 1030 1035 1040
Val Ile Gly Asp Ser Leu Arg Leu Arg Gln Val Ile Thr Asn Leu Val
1045 1050 1055
Gly Asn Ala Ile Lys Phe Thr Pro Ser Lys Pro Asn Lys Lys Gly Met
1060 1065 1070
Val Cys Leu Ser Cys Lys Leu Ile Ser Met Asp Glu Gln Asn Val Thr
1075 1080 1085
Val Arg Phe Cys Val Glu Asp Thr Gly Ile Gly Ile Lys Gln Asp Lys
1090 1095 1100
Leu Ala Ile Ile Phe Asp Thr Phe Cys Gln Ala Asp Gly Ser Thr Thr
1105 1110 1115 1120

Arg Glu Tyr Gly Gly Thr Gly Leu Gly Leu Ser Ile Ser Lys Arg Leu
1125 1130 1135

Val Ser Leu Met Asn Gly Gln Met Trp Val Glu Ser Glu Val Gly Val
1140 1145 1150

Gly Ser Arg Phe Tyr Phe Thr Ile Thr Ala Glu Ile Ser Arg Pro Asn
1155 1160 1165

Met Ala Gln Ser Leu Gln Lys Val Ala Ile Tyr Lys Glu Arg Thr Ile
1170 1175 1180

Leu Phe Val Asp Thr Leu Gly Asp Arg Ser Gly Val Ala Glu Arg Ile
1185 1190 1195 1200

Glu Glu Leu Gln Leu Arg Pro Phe Val Val Arg Asp Ile Ser Gln Val
1205 1210 1215

Ala Asp Lys Ala Lys Ile Pro Phe Ile Asp Thr Val Ile Val Asp Ser
1220 1225 1230

Leu Glu Val Thr Glu Lys Leu Arg Glu Leu Asp His Leu Arg Tyr Thr
1235 1240 1245

Pro Ala Val Leu Leu Thr Pro Val Met Pro Arg Leu Asn Leu Thr Trp
1250 1255 1260

Cys Leu Glu Asn Phe Ile Ser Gly His Val Ala Thr Pro Ser Ser Leu
1265 1270 1275 1280

Asp Asp Leu Ala Glu Ala Leu Ala Lys Gly Leu Glu Ala Asn Ala Ser
1285 1290 1295

Gln Pro Glu Val Thr Pro Ser Asp Val Ala Tyr Asp Ile Leu Leu Ala
1300 1305 1310

Glu Asp Asn Val Val Asn Gln Arg Val Ala Val Lys Ile Leu Glu Lys
1315 1320 1325

Phe Gly His Thr Val Gln Ile Ala Glu Asn Gly Gln Phe Ala Val Asp
1330 1335 1340
Ala Val Lys Ala Arg Tyr Glu Gln Glu Lys Met Phe Asp Val Ile Leu
1345 1350 1355 1360
Met Asp Val Ser Met Pro Phe Met Gly Gly Met Glu Ala Thr Glu Ile
1365 1370 1375
Ile Arg Ala Phe Glu Lys Glu Lys Gly Ile Arg Arg Thr Pro Ile Ile
1380 1385 1390
Ala Leu Thr Ala His Ala Met Ile Gly Asp Arg Glu Arg Cys Ile Gln
1395 1400 1405
Ala Gly Met Asp Glu His Val Thr Lys Pro Leu Arg Arg Thr Asp Leu
1410 1415 1420
Val Ser Ala Ile Lys Arg Leu Val Thr Pro His Gly Ala His
1425 1430 1435

<210> 69
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<212> DNA
<213> Thanatephorus cucumeris

<220>
<221> CDS
<222> (1)..(4317)

<400> 69

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Met Ala Gly Thr Thr Gly Gly His Pro Phe Thr Ala His Leu Val Ala
1 5 10 15

gtg ctg agt atc tat gag tta gga ccg gga cga cca gtg cgc gca ctg 96
Val Leu Ser Ile Tyr Glu Leu Gly Pro Gly Arg Pro Val Arg Ala Leu
20 25 30

ccg acc cgg agc tca cat tcc cat tcc tct tcc ggt tcc cgc cat gcg 144
Pro Thr Arg Ser Ser His Ser His Ser Ser Ser Gly Ser Arg His Ala
35 40 45

cgt gcg ctg tct gtg ccg ccg ttc cca cca ccg cca ccg atg tct ccg 192
Arg Ala Leu Ser Val Pro Pro Phe Pro Pro Pro Pro Pro Met Ser Pro
50 55 60

ccg aac gca ccg atc gac tac gta ggc gct gct ccg ctg ccc cga tac 240
Pro Asn Ala Pro Ile Asp Tyr Val Gly Ala Ala Pro Leu Pro Arg Tyr
65 70 75 80

gat gga ccg cgt gac tgg cag acg gat gcg gtc gag cga gca ctg ggc 288
Asp Gly Pro Arg Asp Trp Gln Thr Asp Ala Val Glu Arg Ala Leu Gly
85 90 95

cgt gtt gcc gcg cgg atg tac gcg gcc gag gcc cag ctg cag gac ctg 336
Arg Val Ala Ala Arg Met Tyr Ala Ala Glu Ala Gln Leu Gln Asp Leu

100 105 110

ctg agc cgc gag tcg agc aca tcc acc ccc gat ccc gct ctc tcg ccc 384
Leu Ser Arg Glu Ser Ser Thr Ser Thr Pro Asp Pro Ala Leu Ser Pro
115 120 125

cgc tcc aac ggc ctc aaa aaa cgc aga gag aac ccg gga aca ccc gat 432
Arg Ser Asn Gly Leu Lys Lys Arg Arg Glu Asn Pro Gly Thr Pro Asp
130 135 140

gag cgc gat ccg tgg cag act gtg cgc ttt caa gag gtc ggt gac cag 480
Glu Arg Asp Pro Trp Gln Thr Val Arg Phe Gln Glu Val Gly Asp Gln
145 150 155 160

gac atg gat ccc gag cca gac acc cct gtt gcc cgc ccc aag gac aag 528
Asp Met Asp Pro Glu Pro Asp Thr Pro Val Ala Arg Pro Lys Asp Lys
165 170 175

gtc aag cct ggt acc att gac ctg agt aca ctc tcc cag ccc act ccg 576
Val Lys Pro Gly Thr Ile Asp Leu Ser Thr Leu Ser Gln Pro Thr Pro
180 185 190

ctc tcc aag gtg gcc acg gac aat ccg gtg ctg ccc aag cct ggt ccc 624
Leu Ser Lys Val Ala Thr Asp Asn Pro Val Leu Pro Lys Pro Gly Pro
195 200 205

cgc agc gca ccc acc agc agc gtc gga tcc atc atg cct ccc ttc acg 672
Arg Ser Ala Pro Thr Ser Ser Val Gly Ser Ile Met Pro Pro Phe Thr
210 215 220

tgc cac tcg tgc gga cgc ccc atg cag ggc ccc gct gcc ccc gat gtc 720
Cys His Ser Cys Gly Arg Pro Met Gln Gly Pro Ala Ala Pro Asp Val
225 230 235 240

ata cac gca ccc ggt ccc ctc gac gtt gtc acc cct gca ctt ggc atg 768
Ile His Ala Pro Gly Pro Leu Asp Val Val Thr Pro Ala Leu Gly Met
245 250 255

ggc ctc ggt ctc tct gac cat ggc gct gcc gag ctc aga cag aaa ctt 816
Gly Leu Gly Leu Ser Asp His Gly Ala Ala Glu Leu Arg Gln Lys Leu
260 265 270

ggc ttt ggc gat cac gaa gac gac acc ggt agt ccc ctt gtt ctc ccc 864
Gly Phe Gly Asp His Glu Asp Asp Thr Gly Ser Pro Leu Val Leu Pro
275 280 285

cct ggc cct ctc agt gct gct gcc ttt gag agc gct cca ggc atg tcc 912
Pro Gly Pro Leu Ser Ala Ala Ala Phe Glu Ser Ala Pro Gly Met Ser
290 295 300

gcc gtc gaa gaa ctc aag ctg ctc aag gcc cag gtc cag gat gtc gct 960
Ala Val Glu Glu Leu Lys Leu Leu Lys Ala Gln Val Gln Asp Val Ala

305 310 315 320

cgt gta tgc aag gcc gtc gcc gag ggt gat ttg tct caa aag att acc 1008
Arg Val Cys Lys Ala Val Ala Glu Gly Asp Leu Ser Gln Lys Ile Thr
325 330 335

gtc ccc gtt caa ggt ccc gtc atg gtc cag ctc aag gat gtc atc aac 1056
Val Pro Val Gln Gly Pro Val Met Val Gln Leu Lys Asp Val Ile Asn
340 345 350

acc atg gtc gat aaa cta ggc agg ttt gcg cag gag gtc act cgt gtc 1104
Thr Met Val Asp Lys Leu Gly Arg Phe Ala Gln Glu Val Thr Arg Val
355 360 365

tcg ctc gaa gtc gga act gaa ggc cgg ctc ggt ggt cag gcc att gtt 1152
Ser Leu Glu Val Gly Thr Glu Gly Arg Leu Gly Gly Gln Ala Ile Val
370 375 380

cgc gat gtc cgc gga aca tgg agc gaa ctc aca acc gtc gtc aat cgt 1200
Arg Asp Val Arg Gly Thr Trp Ser Glu Leu Thr Thr Val Val Asn Arg
385 390 395 400

ctc gcc gct aat ctc aca agc cag gtc cgg gga atc gca gaa gtc acc 1248
Leu Ala Ala Asn Leu Thr Ser Gln Val Arg Gly Ile Ala Glu Val Thr
405 410 415

aag gca gtc gcc aag ggc gat ctc tcc aaa caa atc ggc gtc gat gca 1296
Lys Ala Val Ala Lys Gly Asp Leu Ser Lys Gln Ile Gly Val Asp Ala
420 425 430

aaa ggt gaa ata ttg gaa ttg aag aat acg gtt aat acc atg gtc gtc 1344
Lys Gly Glu Ile Leu Glu Leu Lys Asn Thr Val Asn Thr Met Val Val
435 440 445

cgg ttg cgt atg ttt gca ggc gaa gtc acc cga gtc gcg ctc gat gtc 1392
Arg Leu Arg Met Phe Ala Gly Glu Val Thr Arg Val Ala Leu Asp Val
450 455 460

ggc agt cgt ggt att cta ggc ggt cag gct tat gtc ccg gat gtc gag 1440
Gly Ser Arg Gly Ile Leu Gly Gly Gln Ala Tyr Val Pro Asp Val Glu
465 470 475 480

ggt gtt tgg caa gag ttg acg gat aat gta aat cgc atg tgc tcc aat 1488
Gly Val Trp Gln Glu Leu Thr Asp Asn Val Asn Arg Met Cys Ser Asn
485 490 495

ttg acc aac caa gtc cgt tcg att gcg ctc gtt act acc gcc gtc gcc 1536
Leu Thr Asn Gln Val Arg Ser Ile Ala Leu Val Thr Thr Ala Val Ala
500 505 510

gag ggt gac ctc aca cgt aaa atc gaa att gaa gtc gag ggc gaa atg 1584
Glu Gly Asp Leu Thr Arg Lys Ile Glu Ile Glu Val Glu Gly Glu Met

515 520 525

ttg acg ctc aag aat acg gta aac agc atg gtg gac cag ctt tcg acg 1632
Leu Thr Leu Lys Asn Thr Val Asn Ser Met Val Asp Gln Leu Ser Thr
530 535 540

ttt gcg agc gaa gtc acg cgg gtc gcg ctc gag gtt ggc tcg atg ggt 1680
Phe Ala Ser Glu Val Thr Arg Val Ala Leu Glu Val Gly Ser Met Gly
545 550 555 560

ata ctc ggt ggt cag gcg cag gtc gag ggt gta aaa gga act tgg gcc 1728
Ile Leu Gly Gly Gln Ala Gln Val Glu Gly Val Lys Gly Thr Trp Ala
565 570 575

gac ttg acg agg aat gtg aat aat atg gcg tcc aat cta acc aat caa 1776
Asp Leu Thr Arg Asn Val Asn Asn Met Ala Ser Asn Leu Thr Asn Gln
580 585 590

gtc cgt tcg atc gcc aag gtc acg acg gcc gtc gcg cac ggt gac ctg 1824
Val Arg Ser Ile Ala Lys Val Thr Thr Ala Val Ala His Gly Asp Leu
595 600 605

cgg cag ttt gtc gaa gtc gat gtc cag gga gag atg ctc atg ttg aag 1872
Arg Gln Phe Val Glu Val Asp Val Gln Gly Glu Met Leu Met Leu Lys
610 615 620

aac acg gtg aat agc atg gtg gct cag ctc gat acg ctc gcg agc gag 1920
Asn Thr Val Asn Ser Met Val Ala Gln Leu Asp Thr Leu Ala Ser Glu
625 630 635 640

gtg tcg cgt gtc gcg ctc gag gtc ggt atc gag ggt cga ctc ggt gga 1968
Val Ser Arg Val Ala Leu Glu Val Gly Ile Glu Gly Arg Leu Gly Gly
645 650 655

cag gct gtg gtt cag ggt gtg gag ggt gtg tgg aag gtt tta acg gac 2016
Gln Ala Val Val Gln Gly Val Glu Gly Val Trp Lys Val Leu Thr Asp
660 665 670

aat gtc aac ttg atg gct ctg aat ctg acg acc caa gtg cgg tct att 2064
Asn Val Asn Leu Met Ala Leu Asn Leu Thr Thr Gln Val Arg Ser Ile
675 680 685

gcg gct gtg acg act gcc gtg gcg cgt ggt gac ctt agc aag aat atc 2112
Ala Ala Val Thr Thr Ala Val Ala Arg Gly Asp Leu Ser Lys Asn Ile
690 695 700

gat gtc gat gtc aag ggc gag att ttg gat ttg aag att acg gtc aat 2160
Asp Val Asp Val Lys Gly Glu Ile Leu Asp Leu Lys Ile Thr Val Asn
705 710 715 720

cgc atg acg gat agt ttg cgg ata ttc gct gct gaa gtg act cgt gtc 2208
Arg Met Thr Asp Ser Leu Arg Ile Phe Ala Ala Glu Val Thr Arg Val

725 730 735

gcg cgc gag gtc ggt acg ctc gga cga ctc ggc gga cag gcg ttt gtt 2256
Ala Arg Glu Val Gly Thr Leu Gly Arg Leu Gly Gly Gln Ala Phe Val
740 745 750

cct ggt gtg gct ggc gtg tgg aag gat ttg acg gat aat gtg aat gtt 2304
Pro Gly Val Ala Gly Val Trp Lys Asp Leu Thr Asp Asn Val Asn Val
755 760 765

atg gct gcc aat ttg acg ttg caa gta cga gct att gcc cga gtc aca 2352
Met Ala Ala Asn Leu Thr Leu Gln Val Arg Ala Ile Ala Arg Val Thr
770 775 780

acg gcc gtg tcg gtc gga gac ttg acg acc aag gtc gaa ggc atc gat 2400
Thr Ala Val Ser Val Gly Asp Leu Thr Thr Lys Val Glu Gly Ile Asp
785 790 795 800

gtc gcg ggt gaa atc ttg gat ctc gtc aac acg atc aac gga atg gtg 2448
Val Ala Gly Glu Ile Leu Asp Leu Val Asn Thr Ile Asn Gly Met Val
805 810 815

gac cag ctc gcc gtg ttt gcg gcc gag gtc acg agg gtc gca cgc gaa 2496
Asp Gln Leu Ala Val Phe Ala Ala Glu Val Thr Arg Val Ala Arg Glu
820 825 830

gtc gga acc gag ggt cgg ttg ggt gtt cag gct cgc gtc gaa ggt atg 2544
Val Gly Thr Glu Gly Arg Leu Gly Val Gln Ala Arg Val Glu Gly Met
835 840 845

caa ggc agc tgg cag gcg att acc gta tct gta aac acg atg gct gcc 2592
Gln Gly Ser Trp Gln Ala Ile Thr Val Ser Val Asn Thr Met Ala Ala
850 855 860

aac ttg acg tcc caa gtg cgt ggg ttt gcg caa atc tcg gca gcg gcg 2640
Asn Leu Thr Ser Gln Val Arg Gly Phe Ala Gln Ile Ser Ala Ala Ala
865 870 875 880

acc gac gga gac ttt acg cgc ttc atc acg gtc gaa gcg agc gga gag 2688
Thr Asp Gly Asp Phe Thr Arg Phe Ile Thr Val Glu Ala Ser Gly Glu
885 890 895

atg gac tcg ctc aag acg cag atc aat cag atg gtg tac aac ctc cgg 2736
Met Asp Ser Leu Lys Thr Gln Ile Asn Gln Met Val Tyr Asn Leu Arg
900 905 910

gag agt att cag agg aac acg gct gcg cgt gag gct gct gag ctt gcg 2784
Glu Ser Ile Gln Arg Asn Thr Ala Ala Arg Glu Ala Ala Glu Leu Ala
915 920 925

aat cgg tcc aag tcc gag ttc ctt gcc aac atg tcg cac gag att cga 2832
Asn Arg Ser Lys Ser Glu Phe Leu Ala Asn Met Ser His Glu Ile Arg

930 935 940

acg ccg atg aac ggg att att ggc atg acg gat ctc acg ctt gat acc 2880
Thr Pro Met Asn Gly Ile Ile Gly Met Thr Asp Leu Thr Leu Asp Thr
945 950 955 960

gaa ctt aca cgg acg caa aaa gaa aac ttg ttg ctc gtt cac cag ctc 2928
Glu Leu Thr Arg Thr Gln Lys Glu Asn Leu Leu Leu Val His Gln Leu
965 970 975

gcc aag tct cta ttg ctt att atc gat gat att ctt gat att tcc aag 2976
Ala Lys Ser Leu Leu Leu Ile Ile Asp Asp Ile Leu Asp Ile Ser Lys
980 985 990

atc gag gct ggc agg atg acc atg gaa caa gtc acg tat tct ctc cgc 3024
Ile Glu Ala Gly Arg Met Thr Met Glu Gln Val Thr Tyr Ser Leu Arg
995 1000 1005

ggt act gca ttc ggt atc ctc aag acc ctt gtc gtc cgg gct cac caa 3072
Gly Thr Ala Phe Gly Ile Leu Lys Thr Leu Val Val Arg Ala His Gln
1010 1015 1020

caa aat ctc aac ctg ttc tac gaa gtc gat ccc gag att ccg gac caa 3120
Gln Asn Leu Asn Leu Phe Tyr Glu Val Asp Pro Glu Ile Pro Asp Gln
1025 1030 1035 1040

gtc att ggc gat tcg ctc cgt ctg cga caa gtc att acc aac ctc gtc 3168
Val Ile Gly Asp Ser Leu Arg Leu Arg Gln Val Ile Thr Asn Leu Val
1045 1050 1055

gga aac gct atc aag ttc act ccc agc aag ccc aac aaa aag ggc atg 3216
Gly Asn Ala Ile Lys Phe Thr Pro Ser Lys Pro Asn Lys Lys Gly Met
1060 1065 1070

gtc tgc ctc tcg tgc aag ctc atc tcg atg gac gag cag aat gtg acg 3264
Val Cys Leu Ser Cys Lys Leu Ile Ser Met Asp Glu Gln Asn Val Thr
1075 1080 1085

gtt cgg ttc tgt gtc gag gac acg ggt atc ggt atc aag cag gat aaa 3312
Val Arg Phe Cys Val Glu Asp Thr Gly Ile Gly Ile Lys Gln Asp Lys
1090 1095 1100

ctc gcg atc atc ttt gat acg ttc tgt caa gcc gat ggg tcc acg act 3360
Leu Ala Ile Ile Phe Asp Thr Phe Cys Gln Ala Asp Gly Ser Thr Thr
1105 1110 1115 1120

cgt gaa tac ggt ggt acc ggt ctc ggc ttg tcc atc tcg aaa cga ctc 3408
Arg Glu Tyr Gly Gly Thr Gly Leu Gly Leu Ser Ile Ser Lys Arg Leu
1125 1130 1135

gtg tct ctg atg aat ggc caa atg tgg gtc gag tcc gag gtc gga gtc 3456
Val Ser Leu Met Asn Gly Gln Met Trp Val Glu Ser Glu Val Gly Val

1140 1145 1150

ggg tcc cgc ttc tac ttt acg atc acc gcc gaa atc tcc cgg ccg aac 3504
Gly Ser Arg Phe Tyr Phe Thr Ile Thr Ala Glu Ile Ser Arg Pro Asn
1155 1160 1165

atg gcg caa agt ctg caa aag gtc gcg atc tac aag gag cgc acg atc 3552
Met Ala Gln Ser Leu Gln Lys Val Ala Ile Tyr Lys Glu Arg Thr Ile
1170 1175 1180

ttg ttt gtc gat act ctg ggc gac cgg tcg ggt gtg gcg gag cgt atc 3600
Leu Phe Val Asp Thr Leu Gly Asp Arg Ser Gly Val Ala Glu Arg Ile
1185 1190 1195 1200

gaa gag ctg cag ctg cgt ccg ttt gtc gtg cgg gat atc agc cag gtg 3648
Glu Glu Leu Gln Leu Arg Pro Phe Val Val Arg Asp Ile Ser Gln Val
1205 1210 1215

gcg gac aag gcc aag att ccg ttt atc gat acg gtg att gtg gat tcg 3696
Ala Asp Lys Ala Lys Ile Pro Phe Ile Asp Thr Val Ile Val Asp Ser
1220 1225 1230

ctc gag gtg act gag aaa ttg cgc gag ttg gat cat ttg agg tat acc 3744
Leu Glu Val Thr Glu Lys Leu Arg Glu Leu Asp His Leu Arg Tyr Thr
1235 1240 1245

ccg gcc gtg ctc ttg acg cca gtt atg ccc cga ctg aat ctg acg tgg 3792
Pro Ala Val Leu Leu Thr Pro Val Met Pro Arg Leu Asn Leu Thr Trp
1250 1255 1260

tgt ctt gag aac ttt atc tcg ggt cat gtc gcg acc ccg tct tcg ctc 3840
Cys Leu Glu Asn Phe Ile Ser Gly His Val Ala Thr Pro Ser Ser Leu
1265 1270 1275 1280

gac gat ctt gcc gag gcg ctc gca aag gga ctg gaa gcc aac gca tct 3888
Asp Asp Leu Ala Glu Ala Leu Ala Lys Gly Leu Glu Ala Asn Ala Ser
1285 1290 1295

cag ccc gag gtt acg ccc agc gac gtt gcg tac gac att cta ctg gcc 3936
Gln Pro Glu Val Thr Pro Ser Asp Val Ala Tyr Asp Ile Leu Leu Ala
1300 1305 1310

gaa gac aat gtt gtc aac caa cgt gtg gcc gtc aag att ctc gaa aag 3984
Glu Asp Asn Val Val Asn Gln Arg Val Ala Val Lys Ile Leu Glu Lys
1315 1320 1325

ttt ggt cac acg gtt cag att gcc gag aat gga cag ttt gcg gtc gac 4032
Phe Gly His Thr Val Gln Ile Ala Glu Asn Gly Gln Phe Ala Val Asp
1330 1335 1340

gct gtc aag gct cga tac gaa caa gag aag atg ttt gat gtc att ctt 4080
Ala Val Lys Ala Arg Tyr Glu Gln Glu Lys Met Phe Asp Val Ile Leu

1345 1350 1355 1360

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Met Asp Val Ser Met Pro Phe Met Gly Gly Met Glu Ala Thr Glu Ile
1365 1370 1375

att cgc gcg ttt gag aag gaa aag ggc atc cgc cgc acg cct att atc 4176
Ile Arg Ala Phe Glu Lys Glu Lys Gly Ile Arg Arg Thr Pro Ile Ile
1380 1385 1390

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Ala Leu Thr Ala His Ala Met Ile Gly Asp Arg Glu Arg Cys Ile Gln
1395 1400 1405

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Ala Gly Met Asp Glu His Val Thr Lys Pro Leu Arg Arg Thr Asp Leu
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acg ctt gat acc gaa ctt aca cgg acg caa aaa gaa aac ttg ttg ctc 96
Thr Leu Asp Thr Glu Leu Thr Arg Thr Gln Lys Glu Asn Leu Leu Leu

20 25 30

gtt cac cag ctc gcc aag tct cta ttg ctc att atc gat gat att ctt 144
Val His Gln Leu Ala Lys Ser Leu Leu Leu Ile Ile Asp Asp Ile Leu
35 40 45

gat att tcc aag atc gag gct ggc agg atg acc atg gaa caa gtc acg 192
Asp Ile Ser Lys Ile Glu Ala Gly Arg Met Thr Met Glu Gln Val Thr
50 55 60

tat tct ctc cgc ggc acc gca ttc ggt atc ctc aag acc ctt gtc gtc 240
Tyr Ser Leu Arg Gly Thr Ala Phe Gly Ile Leu Lys Thr Leu Val Val
65 70 75 80

cgg gct cac caa caa aat ctc aac ctg ttc tac gaa gtc gat ccc gag 288
Arg Ala His Gln Gln Asn Leu Asn Leu Phe Tyr Glu Val Asp Pro Glu
85 90 95

att ccg gac caa gtc att ggt gat tcg ctc cgt ctg cga caa gtc att 336
Ile Pro Asp Gln Val Ile Gly Asp Ser Leu Arg Leu Arg Gln Val Ile
100 105 110

acc aac ctc gtt gga aac gcc atc aag ttc aca gag 372
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Val His Gln Leu Ala Lys Ser Leu Leu Leu Ile Ile Asp Asp Ile Leu
        35                  40                  45
Asp Ile Ser Lys Ile Glu Ala Gly Arg Met Thr Met Glu Gln Val Thr
    50                  55                  60
Tyr Ser Leu Arg Gly Thr Ala Phe Gly Ile Leu Lys Thr Leu Val Val
65                  70                  75                  80
Arg Ala His Gln Gln Asn Leu Asn Leu Phe Tyr Glu Val Asp Pro Glu
                85                  90                  95
Ile Pro Asp Gln Val Ile Gly Asp Ser Leu Arg Leu Arg Gln Val Ile
            100                 105                 110
Thr Asn Leu Val Gly Asn Ala Ile Lys Phe Thr Glu
        115                 120
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